US-09-186-342-2.rag

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed May 31 11:03:21 2000; MasPar time 8.27 Seconds 638.314 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-186-342-2 (1-223) from US09186342.pep 1686 Title: Description: Perfect Score:

1 MRVSGVLRLLALIFAIVTTW......KYEGWPELLEMEGCMPPKPF 223 Sequence:

PAM 150 Gap 11 Scoring table:

188963 seqs, 23686106 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq36 1:geneseqp

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Variance 140.762; scale 0.235

Mean 33.108;

Statistics:

SUMMARIES

Pred. No.	1.51e-153	2.59e-84	2.59e-84	2.45e+00	6.95e+00	2.28e+01	2.28e+01	2.70e+01	2.70e+01	3.77e+01	3.77e+01	3.77e+01	4.4e+01	4.44e+01	4.44e+01	4.44e+01	4.44e+01	6.17e+01	6.17e+01	6.17e+01	5.24e+01	5.24e+01	6.17e+01
Description	Protein encoded by a c		Human colon specific q	DmORF1 potassium chann	Human mitochondrial is	Sequence of yellow tai	Gentian flavonoid 3'-h	Human nuclear protein	Amino acid sequence of	Haemin-binding protein	Haemin-binding protein	Heamin-binding protein	Bovine Somatotropin an	Bovine Somatotropin an	Bovine growth hormone	HUG-Br1.	HUG-Br2.	Bovine Somatotropin an	Yellow tail/fin tuna q	Yellowtail tuna growth	Bovine growth hormone	Bovine growth hormone	Staphylococcus aureus
ID	W80475	W46878	W06547	R97984	W48720	P81244	W35714	W62596	W80950	R42381	R42379	R42374	R10967	R10955	W40449	R26153	R26154	R10958	W27340	W25120	R72115	W40457	W77603
DB	: -	1	Н	Н	Н	-	Н	Н	-	Н	Н	Н	Н	٦		Н	Н	н	Н	Н	П	Н	Н
% Query Match Length	223	135	135	618	993	187	476	642	642	146	176	178	191	191	217	533	534	191	204	204	217	217	275
% Query Match	100.0	58.9	58.9	6.4	0.9	9.6	5.6	5.6	9.6	5.5	5.5	5.5	5.4	5.4	5.4	5.4	5.4	5.3	5.3	5.3	5,3	5.3	5.3
Score	1686	993	993	108	102	. 95	95	94	94	92	92	92	91	91	91	91	91	83	83	83	90	90	88
Result No.		~	m	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

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Gaps

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Score 1686; DB 1; Length 223; Pred. No. 1.51e-153; 0; Mismatches 0; Indels

Query Match 100.0%; Best Local Similarity 100.0%; Matches 223; Conservative

g Óλ q

61 PANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDM 120

1 MRVSGVLRLLALIFALVTTWMFIRSYMSFSMKTIRLPRWLASPTKEIQVKKYKCGLIKPC 60

5.24e+01	6.17e+01	6.17e+01	6.17e+01	6.17e+01	6.17e+01	6.17e+01	6.17e+01	7.27e+01	7.27e+01	7.27e+01	8.55e+01	8.55e+01	7.27e+01	7.27e+01	7.27e+01	7.27e+01	8.55e+01	8.55e+01	8.55e+01	7.27e+01	1.00e+02
Pyridine nucleotide tr	Mitochondrial glycerol	Glycerol-3-phosphate d	Klebsiella pneumoniae	The gibbon ape leukemi	GALV receptor protein.	Human gibbon ape leuka	Human sodium-lithium c	Amino acid sequence of	Sequence of ovine grow	Ovine growth hormone.	Ovine growth hormone.	Recombinant Human Soma	Ovine pre-growth hormo	Ovine growth hormone-1	Goat growth hormone pr	H. pylori GHPO 1479 pr	H. pylori ORF 29qe3032	Cyclomaltodextrin qluc	Sequence of cyclomalto	Peripheral nervous sys	GC-A.
W69359	W57326	W30682	W60257	M96998	R72969	R10848	W70498	W59885	P60014	R35432	R40169	R03253	P40015	R05794	P90914	W98535	W55528	R10052	R06110	R92316	R38862
7	7	-	7	Н	7	٦	7	٦	7	П	7	7	7	7	7	7	-	٦	П	٦	1
462	614	614	614	619	619	619	619	166	190	191	191	194	217	217	217	418	418	713	713	1835	1029
5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.2	5.5	5.2	5.2	5.3	5.2	2.5	5.2	•	5.2	5.2	5.2	5.2	5.1
06	8	89	88	83	83	89	68	88	88	88	87	87	88	88	88	88	87	87	87	88	98
24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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ID DETAILS OF SECONDARY OF SECO

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                                                                                                                                                                                                                                                                                                                                                                                                                   89 MSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSGDVMHLVKFLKEIPGGALVLVASYDD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKDLRGKSPFEQFLKNSPDTNKYEGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potassium channel genes from Drosophila melanogaster and Caenorhabditis elegans - useful in assaying substances to determine effects of cell growth, and in inhibiting nematode and insect pests Claim 26, Page 37-39; 79pp; English.
This potassium channel sequence is encoded by the DmORFI gene from Drosophila melanogaster, and has 2 pore-forming domains between 4 hydrophobic transmembrane helix domains. Each pore-forming H5 domains with a VF-G dispettide motif required for potassium septectivity. The protein contains a single N-terminal
                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DMORFI potassium channel protein.

DMORFI; potassium channel; fruitfly; pore-forming domain, transmembrane helix; N-glycosylation site; potassium-agonist; potassium-antagonist; drug screening; insecticide; cafdiac disorder.
              colon cancer metastasis
Claim 8; Fig 4; 60pp; English.
Novel polypeptides (W06545-53) are encoded by cDNA clones (see also
Novel polypeptides (W06545-53) are encoded by cDNA clones (see also
designated CSG1, CSG2, etc., that are primarily expressed in
tissues derived from the colon. Recombinant CSG polypeptides can
be produced in transformed host cells. They are useful diagnostic
markers for colon cancer and for colon cancer metastasis and can
also be used to screen for (ant)agonist cpds. of therapeutic or
diagnostic value. Antibodies raised against the colon specific
                                                                                                                                                                                                                                                                                                                                         Gaps
  which, in non-colon tissue samples, can be used as indication of
                                                                                                                                                                                                                                                                                                                                                                              MSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSGDVMHLVKFLKEIPGGALVLVASYDD
                                                                                                                                                                                                                polypeptides may be used to target colon cancer cells or as part
                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                  Length 135;
                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Pore-forming domain H5-2" 242. .263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Transmembrane domain M3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Tyánsmembrane domain M4"
                                                                                                                                                                                                                                                                                                Score 993; DB 1; 1
Pred. No. 2.59e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "N-glycosylation sixe'
                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 6...27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein; 618 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-1994; US-332312.
(AMCY ) AMERICAN ÇYANAMID CO.
                                                                                                                                                                                                                                                                                              Query Match 58.9%;
Best Local Similarity 100.0%;
Matches 135; Conservative
                                                                                                                                                                                                                                       of a colon cancer vaccine.
Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 PELLEMEGCMPPKPF 135
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/note=
95.
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208..2
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WPI; 96-239450/24.
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                                                                                                                                                                                                                                                                Sednence
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domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 4; 51pp; English.
W46876-80 and W4682-85 represent proteins encoded by colon-specific genes. The polynucleotides encoding these proteins can be used as probes to detect expression of the corresponding human genes, e.g. in diagnostic assays for detecting micrometastases of colon cancer. Recombinant cells containing the polynucleotides can be used to produce the proteins, in order that antibodies can be raised and sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
PANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDM 120
                                                         89 MSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSGDVMHLVKFLKEIPGGALVLVASYDD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKDLRGKSPFEQFLKNSPDTNKYEGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 PGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKDLRGKSPFEQFLKNSPDTNKYEGW 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSGDVMHLVKFLKEIPGGALVLVASYDD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human colon specific genes and their expression products - detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colon-specific nucleic acids - useful as probes for detecting colon
                                    121 YSGDVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human colon specific gene CSG4 polypeptide fragment.
Colon specific gene; CSG4; colon cancer; metastasis; diagnosis;
therapy; antibody; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 135;
                                                                                                                                                                                                                                                                      22-JUN-1998 (first entry)
Protein sequence encoded by a colon-specific gene.
Colon-specific gene; probe; detection; expression; human; diagnostic assay; colon cancer; antibody; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                    IGAKDLRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF 223
                                                                                                                                       Score 993; DB 1;
Pred. No. 2.59e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                     standard; Protein; 135 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC. Rosen CA, Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 58.9%;
Best Local Similarity 100.0%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-1997 (first entry)
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06-JUN-1995; U07289.
06-JUN-1995; WO-U07289.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer micrometastases
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97-043054/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98-229823/20.
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N-MEDB; T45883
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                                                                                                                                                                                                                                   W46878
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                                                                                                                181
61
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90 90

ID DDT DDT DDS DDS DDS DDS DDS DDS 3

protein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant proteins, tester strains, etc.

Claim 3; Columns 47-52; 46pp; English.

The present sequence is that of a human mitochondrial isoleucyl-tRNA synthetase. The cDNA encoding for the mitochondrial isoleucyl-tRNA synthetase was isolated from a human T-cell cDNA library. The cDNA can be expressed using expression vectors to produce the corresponding recombinant protein. The protein can be used in assays to test substances known to inhibit the isoleucyl-tRNA synthetase or other tRNA synthetase or pathogenic organisms. Also, expression of the isoleucyl-tRNA synthetase in a tester strain can be useful for testing substances which are capable of inhibiting its activity.
                                                                                                                                                                                                                                                                                     97 FFAFTVCSTVGYGNISPIT-FAGRMIMIAY-SVIGIPVNGILFAGL-GEYFG-RTFEAIY 152
                                                                                                                                                                                                                                                                                                        887 VIEPGLLFEIIEMLQSEETSSTSQ-LN-ELMMASESTLLAQEPREM-TADVIELKGKFLI 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Gaps
                                                                                                                                                                                                                                                        Gaps
       The protein is predicted to
asparagine-linked glycosylation site. The protein is predicted to span the membrane 4 times, with N- and C-termini within the cell, and the glycosylation site and H2 domains on the cell exterior, allowing permeation of the membrane by the potre-forming domains from the outside, a requirement for functional potassium channel formation. The protein may be expressed in a heterologous host cell to assay substances to determine effects on cell growth. Potassium-agonists or determine effects on cell growth.
                                                                                                                                                                                                                                                        ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human isoleucyl-tRNA synthetase DNA - useful for producing recombinant proteins, tester strains, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 993;
                                                                                                                                                                                                                     Score 108; DB 1; Length 618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrial isoleucyl-tRNA synthetase; T-cell; pathogen.
                                                                                                                                                                                                                                  Pred. No. 2.45e+00;
14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Mismatches 23; Indels
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Sequence of yellow tail fish pre-growth hormone pyGH1; somatotropin.
Yellow tail fish.
Rey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 102; DB 1; Pred. No. 6.95e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-1998 (first entry)
Human mitochondrial isoleucyl-tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CANC-) CANCER INST JAPANESE FOUND CANCER. (CUBI-) CUBIST PHARM INC.
KARDA JE, Schimmel PR, Shiba K;
WPI; 98-332142/29.
N-PSDB; V18326.
                                                                                                                                                                                                                                                                                                                                                                            JT 5
W48720 standard; Protein; 993 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P81244 standard; protein; 187 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watch 6.0%;
Local Similarity 30.1%;
nes 22; Conservative
                                                                                                                                                                                                    Query Match
Best Local Similarity 33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-1994; 250852.
06-JUN-1995; US-468557.
27-MAY-1994; US-250852.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIPGGALVLVASY 146
                                                                                                                                                                   etc.
618 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
US5759833-A.
                                                                                                                                                              disorders,
                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
     88888888888888
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PF 23-JUL-1987; 184083.

24-JUL-1987; JP-184083.

RALJUL-1987; JP-18408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This polypeptide comprises gentian flavonoid 3' hydroxylase (F3'H). Its amino acid sequence was deduced from a cDNA clone (see T94664) isolated from a petal cDNA library. F3'H acts on dihydrokaempferol to produce dihydroquercetin and on naringenin to produce eriodictyol. Isolated F3'H nucleic acids (see T94655-65) can be used to provide genetic constructs capable of modulating the hydroxylation of flavonoid compounds in a plant, e.g. by de novo expression, over-expression, antisense inhibition and ribozyme activity. Modulation of F3'H is useful for the manipulation of pigmentation (flavonoids contribute to a range of colours from yellow to red to blue) in plants, especially flowering plants such as petunia, carnation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chrysanthemum, rose, snapdragon, tobacco, cornflower, pelargonium, lisianthus, gerbera, apple, iris, lily, african violet and morning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel flavonoid 3'-hydroxylase(s) from flowering plants - and corresponding DNA, used in the manipulation of pigmentation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 95; DB 1; Length 476; Pred. No. 2.28e+01; 23; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.6%; Score 95; DB 1; Length 187;
Best Local Similarity 29.8%; Pred. No. 2.28e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 SSVLKLLSISYRLVESWEFSSRFLSGGSALRNQISPRLSELKTEIQL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flavonoid 3' hydroxylase; pigmentation; flower colour;
transgenic plant; gentian.
Gentiana triflora Pall. var japonica Hara.
3. .187
/note="185 AA SQ, see CC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 23; Page 181-184; 234pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brugliera F, Holton TA, Michael MZ;
WPI; 97-448691/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W35714 standard; Protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1998 (first entry)
Gentian flavonoid 3'-hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                structural gene amplification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.6%;
Best Local Similarity 24.5%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-1997; AU0124.
01-MAR-1996; AU-008386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FLOR-) FLORIGENE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chrysanthemum, rose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; T94664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9732023-A1.
                                               J63152985-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qlory
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W80950 standard; Protein; 642 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and corresp. DNA
Claim 1; Fig 6; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 40.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNIV SASKATCHEWAN.
RJ, Pfeiffer CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA0135.
US-865050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JUN-1992; US-893424.
04-JUN-1992; US-893426.
29-MAR-1993; US-038287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-1993; US-038288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-1993; US-038719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rioux C, Theisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus somnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 93-351733/44.
                                                                                                                                                                                                                                                                                            WPI; 98-594481/50.
N-PSDB; V68588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         642 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          051082
                                                                                                                                                          WO9845433-A1.
                                                                                                                                      Homo sapiens
                                                                                                                                                                            15-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09321323-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1993
                                                                                                                                                                                                                                                                          Osborne CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harland RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYSA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R42381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This protein comprises a novel human nuclear protein, designated
This protein comprises a novel human nuclear protein, designated
This protein comprises a novel human nuclear protein, designated
This protein comprises a novel human nuclear protein, designated
The (highly expressed in cancer), that appears to be crucial for
normal mitosis. Its amino acid sequence was deduced from an
isolated B cell cDNA clone (see V38564). HEC localises to the
nuclei of interphase cells and redistributes to centromeres during
M phase. Ectopic expression of a mutant HEC containing only the
leucline heptad repeats results in cells being unable to divide more
than once. Inactivation of HEC results in disordered sister
chromatid alignment and separation, and formation of non-viable
cells with multiple, fragment micronuclei. HEC interacts through
its leucine heptad regions with several proteins involved in
itsels, including nek2, sbi.8 and 2 different regulatory subunits
of the 26s proteasome, MSSI and p45. These properties suggest
cattachment to kinetochores, sister chromatic movement, and M phase
                      LRKICSVHLFSSKALDDFQHVRHEEICILIRAIASGGHAPVNLGKLLGVCTTNALARVML 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; V38564.

Muclelca acid encoding human nuclear protein HEC modulating mitosis useful to, e.g control cell malignancies and other cell growth abnormalities at mitosis stage and to produce HEC protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         abnormalities at the cell mitosis stage. HEC peptides are useful in vaccines and may be administered to cells to disrupt chromatid separation and so medulate cell cycle progression (claimed). HEC specific antibodies are useful in purifying native or recombinant HEC and to detect HEC protein/peptides in samples (claimed immunodetection kits are provided). They can also be administered to disorder slater chromatid alignment and separation in an interphase cell, so disrupting mitosis (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                progression to name of the compositions to control cell malignancies and other cell growth abnormalities at the cell mitosis stage. HEC peptides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                               76-001-1998 (first entry)
Human nuclear protein HEC.
HEC gene; highly expressed in cancer; human; nuclear protein; mitosis; cell cycle; cell proliferation; malignancy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 5.6%; Score 94; DB 1; Length 642; Local Similarity 40.5%; Pred. No. 2.70e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            129 VK-FLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 VKDFLKIFTFLYGFLCPSYELPDTKFEEEVPRIFKDLGYPFA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                             148 GRRVFEGDGGENPHADEF-KSMVVEIMVLAGAFN 180
                                                                                                   /label- O-phosphorylated
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                             W62596 standard; Protein; 642 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-1997; U23385.
20-DEC-1996; US-033600.
(TEXA ) UNIV TEXAS SYSTEM.
Chen P, Chen Y, Lee W, Riley DJ;
WPI; 98-377401/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                        Modified_site
                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9827994-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                   antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Best Loca Matches

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RESULT

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New nucleic acid encoding human highly expressed in cancer nuclear protein - used for diagnosis and for modulation of the cell cycle to control malignant and other cell growth abnormalities

Claim 2; Pages 58-61; 75pp; English.

This is the amino acid sequence of a human nuclear protein (HEC) used in the method of the invention to diagnose cell growth abnormalities.

Fragments of HEC are used to detect HEC-encoding nucleic acid, in conventional immunoassays to detect HEC-encoding nucleic acid, in andlate cell cycle progression (by disrupting chromatid separation) and antibodies are used to discrete HEC or peptides. HEC is used to an antibodies are used to discrete acid chromatid alignment and separation in interphase cells, disrupting mitosis, particularly for control of malignancy and other cell growth abnormalities at the mitosis stage. Antibodies can also be used for protein purification, isolate sequences encoding HEC or related proteins; to study HEC distribution in cells and to isolate antigens by immunoprecipitation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
16-FEB-1999 (first entry)
Anino acid sequence of the human nuclear protein.
Human nuclear protein; HEC; cell growth abnormality; hybridisation; amplification; antibody; immunoassay; malignancy; mitosis; antigen; immunoprecipitation; immunisation; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     selected from haemin-binding protein, haemolysin, LppB and LppC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemin-binding protein produced as fusion protein in pGCH5. Haemophilus somnus; immunogenic; haemolysin; LppB; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 94; DB 1; Length 642;
Pred. No. 2.70e+01;
9; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus somnus immunogenic proteins used in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potter AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 VKDFLKIFTFLYGFLCPSYELPDTKFEEEVPRIFKDLGYPFA 163
                                                                                                                                                                                                                                                                                                                                           03-APR-1998; U06727.
04-APR-1997; US-042609.
(TEXA ) UNIV TEXAS SYSTEM.
Allred DC, Chamness GC, Clark GM, Hilsenbeck SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oneumonia; lktA gene; Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pontarollo RA,
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29-MAR-1993;
29-MAR-1993;
                                                                                                                                                       05-APR-1993;
                                                                                                                         28-OCT-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 - JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R10967;
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NAME OF STREET O
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The hmb gene encoding the haemin-binding protein was expressed in the hmb gene encoding the haemin-binding protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene likth coded for by plasmid pha552. The hmb gene fragment was taken from pRAP501 and starts at the codon for the third amino acid residue of ORT. The haemin binding protein can be used in vaccines for preventing or treating H. Sommus infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis and pneumonia in
                          E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lkta coded for by plasmid pAA352. The hmb gene fragment was taken from pRAP504 and starts at the codon for the 33 rd amino acid residue of ORF1. The haemin binding protein can be used in vaccines for preventing or treating H. Somnus infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis and pneumonia in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 KNLPQGAFDAFVSITFNVGCGKM-QKS-TLFKQANQGFTPQLCHQFERWIYAGGKKLNG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNLPQGAFDAFVSITFNVGCGKM-QKS-TLFKQANQGFTPQLCHQFERWIYAGGKKLNG 128
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   The hmb gene encoding the haemin-binding protein was expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus somnus immunogenic proteins used in vaccines - selected from haemin-binding protein, haemolysin, LppB and LppC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemin-binding protein produced as fusion protein in pGCH5. Haemophilus somnus; immunopenic; haemolylsin; LppB8; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; lktA gene; Pasteurella haemolytica.
                                                                                                                                                                                                                                                                                                                                                  Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 92; DB 1; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             19; Indels
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Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potter AA;
                                                                                                                                                                                                                                                                                                                                               Score 92; DB 1; L. Pred. No. 3.77e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 176 AA.
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29-MAR-1993; US-038287.
29-MAR-1993; US-038288.
29-MAR-1993; US-038119.
(UXSA-) UNIV SASKATCHEWAN.
Harland RJ, Pfeiffer CG, P
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17; Conservative
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larity 28.8%;
Conservative
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09-APR-1992; US-865050.
04-JUN-1992; US-893424.
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Sequence 146 AA;
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Matches 17; Conser
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les 17; Conser
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WPI; 93-351733/44.
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ID R4
AC R4
DT 19
DE HE
KW H2
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Claim 1; Fig 2: 119pp; English.
A genomic cosmid library of Haemophilus somnus HS25 DNA was screened for clones capable of binding bovine haemin and having haemolytic activity. Positive clones were subcloned various times, resulting in plasmid pRAPPOI, which binds haemin but is not haemolytic. The clone was sequenced and was found to contain several open reading frames, potentially encoding 8 proteins. The haemin binding protein (encoded by the hmb gene) was encoded by ORPI. The protein can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis and pneumonia in vertebrates.
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Replacing Glu at position 126 of bovine somatotropin reduces hydrophobicity and helical stability in the region of the mutation. The analogue-bsr has a lower propensity of the partially denatured protein for aggregation and precipitation during processing. It also has enhanced bloactivity and can be used for enhancing the growth of an animal, e.g. beef cattle or increasing milk production in dairy cows. The mutation was introduced by standard site-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residues 96 to 133 to reduce hydrophobicity or helical stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus somnus immunogenic proteins used in vaccines - selected from haemin-binding protein, haemolysin, LppB and LppC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Ala, Cys, Leu, Gln, His, Lys, Val, Ile,
Phe, Tyr, Trp, Thr, Gly, Ser, Asp, Asn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; haemin-binging protein. Haemophilus somnus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 92; DB 1; Length 178; Pred. No. 3.77e+01; 18; Mismatches 19; Indels
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Bovine Somatotropin analogue #20.
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17; Conservative
                                                                                                                                                                                                                                                                                                                                                                 (UYSA-) UNIV SASKATCHEWAN.
Harland RJ, Pfeiffer CG,
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10-JUL-1989; US-377926.
                                                                                                                                                                                  US-865050.
US-893424.
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US-038288.
US-038719.
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Peptide
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                                                                                                                                                                                                         93 LSRVFINSLVFGTSDRVY-EKLXDLEEG-ILALMRELEDGTPRAGQILKQTYDKFDTNMR 150
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06-UUL-1998 (first entry)
Bovine growth hormone variant protein K114W.
Growth hormone; wariant; mutant; bovine; antagonist; treatment;
Bos taurus.
Syfthetic.
Syfthetic.
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Replacing Lys at position 114 of bovine somatotropin reduces
hydrophobicity and helical stability in the region of the mutation.
The analogue-bST has a lower propensity of the partially denatured
protein for aggregation and precipitation during processing. It
also has enhanced bloactivity and can be used for enhancing the
growth of an animal, e.g.beef cattle or increasing milk production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Animal somatotropin analogues – have aminoacid changes at residues 96 to 133 to reduce hydrophobicity or helical stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phe, Tyr, Trp, Thr, Gly,
                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in dairy cows. The mutation was introduced by standard site-
directed techniques.
See also R10625-7, R10947-R10954 and R10956-R10968.
                                                                                            Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 91; DB 1; Length 191;
Pred. No. 4.44e+01;
21; Mismatches 32; Indels
                                                                                                                                        Indels
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Bovine Somatotropin analogue #9.
bovine somatotropin; bST; dairy cow; helical stability.
                                                                                          Score 91; DB 1; Leng
Pred. No. 4.44e+01;
21; Mismatches 32;
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Lehrman SR, Havel HA, Plaisted SM, Brems DN;
WPI; 91-051315/07.
directed techniques.
See also R10625-7, R10947-R10966 and R10968.
Sequence 191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Cys, Val, Ile, I
Ser, Asp, Asn, Pro, Ala
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R10955 standard; Protein; 191 AA.
R10955;
                                                                                                                                                                                                                                                                  151 SDDALLKNYGLLSCFRKDL 169
                                                                                                                                                                                                                                                                                                             155 DESRKLFS-DLGSSYAKQL 172
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Best Local Similarity 27.8%;
Matches 22; Conservative
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Best Local Similarity 27.8%;
Matches 22; Conservative
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10-JUL-1989; US-377926.
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Example 5: Page -: 28pp; English.

This sequence represents a variant of bovine growth hormone which alters the mature protein amino acid sequence represented in W37691. This variant is used in a method to detect growth hormone antagonists. Such disorders characterised by excessive or undesirable growth hormone activity, especially diabetic retinopathy, glomerulosclerosis or growth hormone-dependent tumours, and for lowering serum cholesterol levels. Note: This sequence does not appear in the specification but has been constructed from the sequence represented in Figure 1.
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GenCore version 4.5
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May 31, 2000, 17:24:57 ; Search time 78.65 Seconds (without alignments) 3884.101 Million cell updates/sec Run on:

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623170 Total number of hits satisfying chosen parameters:

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N_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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28-JAN-1999 (first entry)
Full length sequence of clone 1281865 corresponding to CS141 sequence.
EST sequence; CS141; gastrointestinal tract; cancer; Barret's esophagus; ulcerative ulcer; gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis; pantreatitis; ss.
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Claim 1; page 92; Il6pp; English.
Claim 1; page 92; Il6pp; English.
Sequences designated CS141. The sequences are isolated from a cDNA library made from gastrointestinal tract tumour and normal tissues. The CS141 gene is useful as a marker for gastrointestinal tract disorders. The methods and products can be used in detecting, diagnosing, staging, monitoring, proprosticating, preventing, or gastrointestinal tract, such as gastrointestinal tract cancers. Barret's esophagus, gastric ulcer, gastrointestinal tract cancers, Edin's disease, ulcerative colitis, pantreatits, leiomyoma, polyps, Grohn's disease, ulcerative colitis, pantreatitis, leiomyoma, polyps, Grohn's disease, ulcerative colitis, pantreatitis, 197 T;
                                                                                                                                                                                                                                                                                                                                                                      nseq
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100.0%; Pred. No. 2.7e-266;
1ve 0; Mismatches 0;
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Best Local Similarity 100.
Matches 941; Conservative
                                                                                                                                                                                                 08-OCT-1998.
31-MAR-1998; UO6337.
31-MAR-1997; US-828489.
(ABBO ) ABBOTT LAB.
                                                                                                                                                              Homo sapiens
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therapy; ss.
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                                                                         agacacaaacaaatacgagggatggccagagctgctggagatggagggctgcatgcccc
                                                                                                  541 AGACACAAACAAATACGAGGGATGGCCAGAGCTGCTGGAGGATGGAGGGCTGCATGCCCCC
                                                                                                                           gaagccattttagggtggctgtggctcttctcagccaggggcctgaagaagctcctgcc
                                                                                                                                                   601 GAAGCCATTITAGGGTGGCTGTGGCTCTTCCTCAGCCAGGGGCCTGAAGAAGCTCCTGCC
                                                481 CATAGGAGCCAAAGACCTCAGGGGTAAAAGCCCCTTTGAGCAGTTCTTAAAGAACAGCCC
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Polynucleotide sequence of a colon-specific gene.
Colon-specific gene; probe; detection; expression; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 515.6; DB 1; Length
Pred. No. 1e-141;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic assays for detecting micrometastases of colon
Recombinant cells containing the polynuclectides can be
produce the polypeptides, in order that antibodies can be
used in further screening or diagnostics. 173 G; 107 's
Sequence 548 BP; 137 A; 128 C; 173 G; 107 's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic assay; colon cancer; antibody; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                  1181 tgcccagacttgagcccaattaaattttatttttgctggta 1221
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06-JUN-1995; 469667.
06-JUN-1995; US-469667.
(HUMA-) HUMAN GENOME SCI INC.
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WPI; 98-229823/20.
P-PSDB; W46878.
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Claim 1; Fig 4; 60pp; English.
13 cDNA clones (745880-92), most of them partial clones, correspond
to human colon specific genes, designated CSG1, CSG2, etc., that
are primarily expressed in tissues derived from the colon. CSG7
and CSG10 show reduced expression in colon cancer cells as compared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to that in normal cells, the remaining genes are overexpressed in colon cancer. The partial CDNA sequences can be used to isolate full-length clones and genomic clones including the complete gene. CSG nucleic acids can be used to produce CSG polypeptides (see also w06545-53) in transformed host cells, as probes to detect disorders
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666 ccagggaccaaaatgaacgatgaaagcaggaaactcttctctgacttggggagttcctac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1997 (first entry)
Human colon specific gene CSG4 cDNA partial clone.
Colon specific gene; CSG4; colon cancer; metastasis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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T45883;
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06-JUN-1995; U07289
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WPI; 97-043054/04.
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Claim 1; Page
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                                                                                                                     546 acgggagctgtgctgggacagaaggcatttgacatgtactctggagatgttatgcaccta
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                                                                                                                                                                          121 GTGAAATTCCTTAAAGAAATTCCGGGGGGGTGCACTGGTGCTGGTGGCCTCCTACGACGAT
                                                                                                                                                                                                                CCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTGGGCAGTTCCTAC
                                                                                                                                                                                                                                   gcaaaacaactgggcttccgggacagctgggtcttcataggagccaaagacctcagggggt
                                                                                                                                                                                                                                                                      ccagggaccaaaatgaacgatgaaagcaggaaactcttctctgacttggggagttcctac
                                                                                                                                                                                                                                            241 GCAAAACAACTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGACCTCAGGGGT
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  metastasis,
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                                              514; DB 1; Length 548;
No. 3e-141;
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                                                                8; Indels
                    107
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Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR, Kratcchvil JD, Roberts-Rapp L, Russell JC, Stroupe SD; WPI; 98-568280/48.
 colon cancer and colon cancer
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Clone 92197992 EST corresponding to CS141 sequence.
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                   172
                                              Score 514; DB
Pred. No. 3e-14
1; Mismatches
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                   129
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                  137 A;
                                              42.1%;
98.0%;
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V63513;
                                           Query Match
Best Local Similarity 98.0
Matches 539; Conservative
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WO9844133.A1.
08-OCT-1998.
31-WAR-1998; U06337.
31-WAR-1997; US-828489.
the colon, partic.
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                  BP;
        therapy.
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Clone 3210629 EST corresponding to CS141 sequence.
EST sequence; CS141; gastrointestinal tract; cancer; Barret's esophagus; gastric ulcer; gastritis; lecimyoma; polyps; Crohn's disease; ulcerative colitis; pantreatitis; ss.
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           Cident 1: regressent a set of contiguous and partially overlapping Engequences designated CS141. The sequences are isolated from a cDNA library made from gastrointestinal tract tumour and normal tissues. The CS141 gene is useful as a marker for gastrointestinal tract disorders. The methods and products can be used in detecting, diagnosing, staging, monitoring, prognosticating, preventing, or determining the predisposition to diseases and conditions of the gastrointestinal tract, such as gastrointestinal tract, such as gastrointestinal tract cancers, Barret's esophagus, gastric ulcer, gastriitis, leiomyoma, polyps, Crohn's disease, ulcerative colitis, pantreatitis.

Sequence 301 BP; 63 A; 92 C; 77 G; 69 T;
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V63504-15 represent a set of contiguous and partially overlapping E sequences are isolated from a cDNA library made from gastrointestinal tract tumour and normal tissues. The CS141 gene is useful as a marker for gastrointestinal tract disorders. The methods and products can be used in detecting, diagnosing, staging, monitoring, prognosticating, preventing, or determining the predisposition to diseases and conditions of the gastrointestinal tract, such as gastrointestinal tract, cancers,
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31-MAR-1997; US-828489.
31-MAD ABDOTT LAB.
Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR,
Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;
WPI; 98-56280/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.4%; Score 286; DB 1; I
100.0%; Pred. No. 1.6e-74;
.1ve 0; Mismatches 0;
1; Page 92; 116pp; English
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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EST sequence; CS141; gastrointestinal tract; cancer; Barret's esophagus;
estric ulcer; gastriis; lelomyoma; polyps; Crohn's disease;
ulcerative colitis; pantreatitis; ss.
                                                                                                                                                                                                                                                                                                   261
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                                                                                                                                                                                                                                             142 cttctccatcgaagcagggaagtgggagcctcgagcctcgggtggaagctgaccccaag 201
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                                                                                                                                                        61
                                                                                                   Gaps
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V63504-15 represent a set of contiguous and partially overlapping ES sequences designated CS141. The sequences are isolated from a cDNA library made from gastrointestinal tract tumour and normal tissues. The CS141 gene is useful as a marker for gastrointestinal tract disorders. The methods and products can be used in detecting, disorders. The methods and products can be used in detecting, determining the predisposition to diseases and conditions of the gastrointestinal tract, such as gastrointestinal tract cancers, Barret's esophagus, gastric ulcer, gastriits, lelomyoma, polyps, Crohn's disease, ulcerative colitis, pantreatitis.
                                                                                                                               aggagggccgtctgtga-gccactacccctccagcaactgggaggtgggactgtcagaag
                                                                                                                                              2 ACGAGGGCCGTCTGTNAGGCCACCACCCTCCAGCAACTGGGAGGTGGGACTGTAGANG
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 Barret's esophagus, gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative colitis, pantreatitis.
Sequence 287 BP; 54 A; 85 C; 87 G; 58 T;
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                                                                        Length
                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                          242 TTGCCATAGTCACGACATGGATGTTTATTCGAAGCTACATGAGCTT 287
                                                                                                                                                                                                                                                                                                                                                          262 ttgccatagtcacgacatggatgtttattcgaagctacatgagctt 307
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100.0%; Pred. No. 8.2e-68;
Live 0; Mismatches 0;
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                                                                       Score 269.4; DB 1
Pred. No. 1.1e-69;
                                                                                                   0; Mismatches
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                                                                     22.1%;
ilarity 98.3%;
Conservative
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31-MAR-1997; US-828489.
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                                                                                     Similarity
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Homo sapiens.
WO9844133-A1.
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                                                                                  Best Local Sim
Matches 281;
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Best Local &
                               Sequence
                                                                       Query Match
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Clone 1735382 EST corresponding to CS141 sequence.
EST sequence; CS141; gastrointestinal tract; cancer; Barret's esophagus; gastric ulcer; gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis; pantreatitis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
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                                                     181 TATGTGCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGGCAGAGGCCT
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tatgtgctttgaagaccgcatgatcatgagtcctgtgaaaaacaatgtgggcagaggcct
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                                                                                                        BP
                                                                                                                                                                                                                                                                                                      standard; cDNA; 251
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W09844133-A1.
08-OCT-1998.
31-MAR-1999; U06337.
31-MAR-1997; US-828489.
(ABBO ) ABBOTT LAB.
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281 gatgtttattcgaagctacatgagcttcagcatgaaaaccatccgtctgccacgctggct 340

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28-JAN-1999 (first entry)
Clone 775762 EST corresponding to CS141 sequence.
EST sequence; CS141; qastrointestinal tract; cancer; Barret's esophagus;
gastric ulcer; gastritis; leiomyoma; polyps; Crohn's disease;
ulcerative colitis; pantreatitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone 2645837 EST corresponding to CS141 sequence.
EST sequence; CS141; gastrointestinal tract; cancer; Barret's esophagus; gastric ulcer; gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis; pantreatitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 acctgctggaccacctcgccttctccatcgaagcagggaagtgggagcctcgagccctcg 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGTGGTCAGCTGGGTCAGGGACCTACGGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pancreating.
Claim 1, Page 90; 116pp; English.
V63504-15 represent a set of contiguous and partially overlapping EX sequences designated CS141. The sequences are isolated from a CDNA library made from gastrointestinal tract tumour and normal tissues. The CS141 gene is useful as marker for gastrointestinal tract disorders. The methods and products can be used in detecting, diagnosing, staging, monitoring, prognosticating, preventing, or determining the predisposition to diseases and conditions of the gastrointestinal tract, such as gastrointestinal tract cancers, Barret's esophagus, gastric ulcar, astrictis, leiomyoma, polyps, Crohn's disease, ulcerative colitis, pantreatitis.
Sequence 233 BP; 44 A; 73 C; 77 G; 39 T;
                                                                                                                                                                                                                                                                                                                              New gastrointestinal tract specific polynucleotides, CS141 - used develop products for the diagnosis and treatment of e.g. cancers, gastric ulcer, gastritis, Crohn's disease, ulcerative colitis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ccgggcaggttgcatctagaggagggccgtctgtga-gccactaccctccagcaactgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGGCCCACTGCATCTAGAGGAGGCCGTCTGTGAGGCCACTACCCCTCCAGCAACTGG
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31-MAR-1997; US-828489.
(ABBOT LAB.
B111ing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 209; DB 1;
Pred. No. 5.3e-52;
0; Mismatches 5
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97.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 17.1
Best Local Similarity 97.4
Matches 223; Conservative
                                                                                                                                                                                      31-MAR-1998; U06337.
31-MAR-1997; US-828489.
                                                                                                                                                                                                                             (ABBO ) ABBOTT LAB.
                                                                                                                          Homo sapiens.
WO9844133-A1.
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                                                                                                                                                                                                                                                                                                        Clone 1807758 EST corresponding to CS141 sequence. EST sequence. CS141; gastrointestinal tract; cancer; Barret's esophagus; gastric ulcer; gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis; pantreatitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V63504.15 represent a set of contiguous and partially overlapping EST sequences designated CS141. The sequences are isolated from a cDNA library made from gastrointestinal tract tumour and normal tissues. The CS141 gene is useful as a marker for gastrointestinal tract disponders. The methods and products can be used in detecting, disponding, staging, monitoring, proponosticating, preventing, or determining the predisposition to diseases and conditions of the gastrointestinal tract, such as gastrointestinal tract cancers, barrointestinal tract, such as gastrointestinal tract cancers, crohn's disease, ulcerative colitis, pantreatitis.

Sequence 228 BP; 63 A; 48 C; 68 G; 49 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 gigaaaaacaaigigggcagaggcciaaacaicgccciggigaaiggaaccacgggagci 554
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               New gastrointestinal tract specific polynucleotides, CS141 - used develop products for the diagnosis and treatment of e.g. cancers, gastric ulcer, gastritis, Crohn's disease, ulcerative colitis or
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100.0%; Pred. No. 1.4e-57;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 91; 116pp; English.
                                                                                                                                                                                                                                          V63510 standard; cDNA; 228 BP
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V63507;
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(ABBO ) ABBOTT LAB.
                                                                                                879
                                                                                                                      241 CTGCATGCCCC 251
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Matches 228; Conserv
                                                                                                  ctgcatgcccc
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181 AAAGNNG 187
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WO9844133-A1.
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                                                                                       Query Match
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                                                                                                        Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barret's esophagus;
disease;
                                                                                    paintential pages 89-90; 116pp; English.
V63504-15 represent a set of contiguous and partially overlapping EST sequences designated CS141. The sequences are isolated from a cDNA library made from gastrointestinal tract tumour and normal tissues. The CS141 gene is useful as a marker for gastrointestinal tract disorders. The methods and products can be used in detecting, disonosing, staging, monitoring, prognosticating, preventing, or determining the predisposition to diseases and conditions of the gastrointestinal tract, such as gastrointestinal tract cancers, Barret's esophagus, gastric ulcer, gastritis, leionyoma, polyps, Crohn's disease, ulcerative colitis, pantreatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                gaggitgggacigicagaagciggcccagggitggitggicagcigggitcagggacciacggc 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 acctgctggaccacctcgccttctccatcgaagcagggaagtgggagcctcgagccctcg 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 ACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAGGAAGTGGGAGCCTCGAGCCTCG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGTGGGACTGTCAGAATCTGGCCCAGGGTGGTCGTCAGCTGGGTCAGGGACCTACGGC 149
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                                                                                                                                                                                                                                                                                                                                                                                   30 CTGGGCCCACTGCATCTAGAGGAGGGCCGTCTGTGAGGNCACTACCCCTCCAGCAACTGG 89
                                                                                                                                                                                                                                                                                                                                                                  cogggcaggttgcatctagagggggggcgtctgtga-gccactacccctccagcaactgg 62
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V63504-15 represent a set of contiguous and partially overlapping E sequences designated CS141. The sequences are isolated from a CDNA library made from gastrointestinal tract tumour and normal tissues. The CS141 gene is useful as a marker for gastrointestinal tract disorders. The methods and products can be used in detecting,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rointestinal tract specific polynucleotides, CS141 - used products for the diagnosis and treatment of e.g. cancers, ulcer, gastritis, Crohn's disease, ulcerative colitis or
                               nseq
                         New gastrointestinal tract specific polynucleotides, CS141 - used develop products for the diagnosis and treatment of e.g. cancers, gastric ulcer, gastritis, Crohn's disease, ulcerative colitis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosing, staging, monitoring, prognosticating, preventing, or determining the predisposition to diseases and conditions of the
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                                                                                                                                                                                                                                                                                                         Length 250;
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                                                                                                                                                                                                                                                                                                                                       9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD; WPI; 98-568280/48.
                                                                                                                                                                                                                                                           42 T;
Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST sequence; CS141; gastrointestinal tract; cancer; gastric ulcer; gastritis; leiomyoma; polyps; Crohn's ulcerative colitis; pantreatitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone 2128334 EST corresponding to CS141 sequence.
                                                                                                                                                                                                                                                                                                      Score 196.4; DB 1;
Pred. No. 2.7e-48;
                                                                                                                                                                                                                                                           78 G;
                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                            81 C;
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                                                                                                                                                                                                                                                                                                          16.1%;
95.5%;
                                                                                                                                                                                                                                                           46 A;
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                                                                                                                                                                                                                                                                                                                                        211; Conservative
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31-MAR-1998; U06337.
31-MAR-1997; US-828489.
(ABBO ) ABBOTT LAB.
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                              250 BP;
                   WPI; 98-568280/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
Homo sapiens.
WO9844133-A1.
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                                                                             pancreatitis
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Clone 1338704 EST corresponding to CS141 sequence.
EST sequence: CS141; gastrointestinal tract; cancer; Barret's esophagus; gastric ulcer; gastriits; lelomyoma; polyps; Crohn's disease; ulcerative colitis; pantreatitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  959 ccggcagggctgaggaggaggaggaggggtgctgcgtggaaggtgctgcaggtccttg 1018
                                                                                                                                                                                                                                                                                                                                                                                                                         EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CCGGCAGGGGCTGAGGAGGAGGAGCAGNGGGTGCTGCGGGAAGGTGCTGCAAGTCCTTG 180
                                                                                                                                                                                                                                                                                                    839 gggatggccagagctgctggagatggaggctgcatgcccccgaagccattttagggtgg 898
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                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New gastrointestinal tract specific polynucleotides, CS141 - used develop products for the diagnosis and treatment of e.g. cancers, gastric ulcer, gastritis, Crohn's disease, ulcerative colitis or
                                                                                                                                                                                                                                                                                                                                ;
gastrointestinal tract, such as gastrointestinal tract cancers, Barret's esophagus, gastric ulcer, gastriits, leiomyoma, polyps, Crohn's disease, ulcerative colltis, pantreatitis, Sequence 187 BP, 35 A; 42 C; 74 G; 33 T;
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                                                                                                                                                                              DB 1; Length 187;
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Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR,
Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;
WPI; 98-568280/48.
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9
                                                                                                                                                                              Score 179.2; DB 1
Pred. No. 2.6e-43;
0; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V63505 standard; cDNA; 250 BP
                                                                                                                                                                                 14.7%;
96.8%;
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Best Local Similarity 95.2
Matches 179; Conservative
                                                                                                                                                                                                                                              Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1998; U06337.
31-MAR-1997; US-828489.
                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                               28-JAN-1999 (first entry)
Clone 775133 EST corresponding to CS141 sequence.
EST sequence: CS141; gastrointestinal tract; cancer; Barret's esophagus; gastric ulcer; gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis; pantreatitis; ss.
                              182
                                                         182
                                                                   V63504-15 represent a set of contiguous and partially overlapping EST sequences designated CS141. The sequences are isolated from a cDNA library made from gastrointestinal tract tumour and normal tissues. The CS141 gene is useful as a marker for gastrointestinal tract disorders. The methods and products can be used in detecting, diagnosing, staging, monitoring, prognosticating, preventing, or determining the predisposition to diseases and conditions of the gastrointestinal tract, such as gastrointestinal tract cancers, crohn's disease, ulcerative colitis, leiomyoma, polyps, crohn's disease, ulcerative colitis, pantreatitis, leiomyoma, polyps, Sequence 273 BP; 49 A; 81 C; 90 G; 46 T;
  gaggtgggactgtcagaagctggcccagggtggtggtcagctgggtcagggacctacggc 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gaggtgggactgtcagaagctggcccagggtggtggtcagctgggtcagggacctacggc 122
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                  GAGGTGGGACTGTCAGANGCTGGCCCAGGGTGGTGGTCAGCTGGGTCAGGGACCTACGGC
                                                       acctgctggaccacctcgccttctccatcgaagcagggaagtgggagcctcgagccctcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CS141 - used
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31-MAR-1997; US-828489.
(ABBO ) ABBOTT LAB.
Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD; WPI; 98-568280/48.
New gastrointestinal tract specific polynucleotides, CS141 - used develop products for the diagnosis and treatment of e.g. cancers, gastric lice, gastritis, Crohn's disease, ulcerative colitis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 273;
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0; Mismatches 12
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                                                                                                                                                                                                      V63504 standard; cDNA; 273 BP.
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Best Local Similarity 93.1
Matches 190; Conservative
                                                                                                            ggtggaag 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New gastrointestinal tract specific polynucleotides, CS141 - used develop products for the diagnosis and treatment of e.g. cancers, gastric ulcer, gastritis, Crohn's disease, ulcerative colitis or
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31-MAR-1997; US-828488.
31-MABC-1997; US-828488.
Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR, Kratcchvil JD, Roberts-Rapp L, Russell JC, Stroupe SD; WPI; 98-568280/48.
                                                                                         28-JAN-1999 (first entry) Clone 92409650 EST corresponding to CS141 sequence. EST sequence; CS141; sequence. CS141: gastridist gastrictis: leiomyoma; polyps; Crohn's ulcerative colitis; pantreatitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.3%; Score 114; DB 1; 1
100.0%; Pred. No. 2.8e-24;
Live 0; Mismatches 0;
standard; cDNA; 123
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Best Local Simi
Matches 114;
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Search completed: May 31, 2000, 19:03:54 Job time: 5937 sec

RESULT

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

May 31, 2000, 17:30:02; Search time 57.43 Seconds (without alignments) 2763.569 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-186-342-1 1221 1 cgcccgggcaggttgcatct.....aaattttattttgctggta 1221

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

230463 seqs, 64992525 residues Searched:

460926 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/FOMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/PCTUS_SOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 6, Appli	Sequence 6, Appli	-	19	Sequence 1, Appli	Sequence 7, Appli	,	Ä	Sequence 2, Appli	8	Sequence 8, Appli	Sequence 33, Appl	19	~			31,	Sequence 1, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 6, Appli	Sequence 7, Appli	Patent No. 5187076	12,	Sequence 1, Appli
SUMMAKIES	ID	US-08-469-667-6	PCT-US95-07289-6	US-08-232-463-14	US-08-665-259-19	US-07-960-389-1	US-07-923-724-7	US-08-609-426A-7	US-08-374-652C-1	US-08-294-189-2	US-08-283-917-8	US-08-961-716-8	US-08-151-574-33	US-08-146-424-19	US-08-693-709-1	US-08-419-448-33	US-08-151-574-31	US-08-419-448-31	US-08-323-443B-1	US-08-190-560-3	US-08-469-277-3	US-08-468-946-3	US-08-468-942-3	US-08-377-292-6	us-07-989-847-7	5187076-5	US-08-365-486A-12	US-07-642-002-1
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ø	Query Match	42.2	42.2	3.8	3.1	5.9	2.8	2.8	2.8	2.8	2.8	2.8	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	5.6	2.6	5.6	5.6	2.6
	Score	51	515.6	46.6	38	35.8	34.4	34.4	34.4	33.8	33.6	33.6	33	33	33	33	33	33	33	32.6	32.6	32.6	32.6	32	32	32	32	32
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US-08-888-077A-31 US-07-951-715A-3 US-08-459-44BA-3 US-07-951-715A-4 US-07-951-715A-8 US-07-951-715A-8 US-08-459-44BA-4 US-08-459-44BA-8 US-08-459-595A-4 US-08-459-595A-8 US-08-459-595A-8 US-08-459-595A-8 US-07-951-715A-12 US-07-951-715A-14 US-07-951-715A-14 US-07-951-715A-14 US-07-951-715A-14	US-U8-459-448A-12 US-08-459-448A-14 US-08-459-448A-27
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331.6 331.6 331.6 331.6 331.6	31.6 31.6 31.6
222 333 333 333 344 444 35 36 37 37 37 37	444 545

ALIGNMENTS

Query Match

42.2%; Score 515.6; DB 2; Length 548;

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999ctgaggaggaggagcaggggggtgctgcgtggaaggtgctgcaggtccttgcacgctg 1025
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Pred. No. 3e-142;
1; Mismatches 7;
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
             TELECOMMUNICATION INFORMATION:
                                           INFORMATION FOR SEQ ID NO: 6: SEQUEBNCE CHARACTERISTICS: LENGTH: 548 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                        42.2%;
98.2%;
                       201-994-1700
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                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA
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                       TELEPHONE:
TELEFAX: 2
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LOCATION:
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; LOCATION:
PCT-US95-07289-6
                                                                                                                                                                 FEATURE:
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                      Indels
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ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
WEDIOM TYPE: Floppy disk
COMPUTER: Parentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: PCT/US95/07289
FILING DATE: PC-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Colon Specific Genes and Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
3e-142;
                   1; Mismatches
         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US95-07289-6; Sequence 6, Application PC/TUS9507289; GENERAL INFORMATION:
        98.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
                 Matches 540; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tgtcgcgcct 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539 TGTCGCGCCT 548
        Best Local Similarity
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                                                                                       546
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868 getgeatgececegaagecattttagggtggetgtggetetteetteetcagecaggggeetga 927
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Patent No. 6028173
GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Connors, Timothy C.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Wan Raay, Terence J.
APPLICANT: Klinger, Katherine W.
APPLICANT: Conversion Conversion of Convers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259 FILING DATE: 17-UN-1996 CLASSIFICATION: 435 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A. REGISTRATION NUMBER: 37,315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.1%; Score 38; DB 5. Best Local Similarity 59.4%; Pred. No. 0.19; Matches 82; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America 2IP: 01701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENZYME CORPORATION
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Patent No. 5705611
GENERAL INFORMATION:
APPLICANT: HAYASHIDA, Kasuhiro;
TITLE OF INVENTION: Human GM-CS;
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: IGS-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-5416
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 6803 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-665-259-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                US-08-665-259-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tectaegeaaaacaactgggetteegggaeagetgggtetteataggageeaaagaeete 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 atgatcatgagtcctgtgaaaaacaatgtgggcagaggcctaaacatcgccctggtgaat 539
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Best Local Similarity 6.0%; Pred. No. 0.0006;
Matches 25; Conservative 213; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30472/114 IMMU
                                                   ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                      EP 91 114 300.6
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BERT, Stephen A.
REGISTRATION NUMBER: 29,768
REPERRINGE/DOCKET NUMBER: 3047;
TELECHONE: (703)836-9300
TELEPAX: (703)8836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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1100 New York Avenue, Suite 600
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Paloheimo, Marja T.
Miettinen-Olnonen, Arja S.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(404..447, 550..1906)
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1169 GAATTGGCCGATACCGTCGAAGCC 1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
TELEPHONE: (202) 371-2560
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Torkkeli, Tuula K. Cantrell, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2363 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 48.03
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                               Washington
                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                            20005
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US-07-923-724-7
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nevalatinen, Helena K.M.
APPLICANT: Paloheimo, Maria T.
APPLICANT: Paloheimo, Maria T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Rambosek, John A.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Maria K.
APPLICANT: Turunen, Maria K.
APPLICANT: Pagerstr m. Richard B.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: In Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 2.9%; Score 35.8; DB 2; Local Similarity 61.1%; Pred. No. 0.61; les 58; Conservative 0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1076 GCTGAGGGGGCTCGGCAGCCTCCACACCAGGC 1110
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                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disc
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System Software 7.1
SOFTWARE: MICTOSOFT WORD 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/960,389
FILING DATE: 07-JAN-1993
CLASSIFCATION: 800
PRIOR APPLICATION NUMBER: S54,745
FILING DATE: 18-UL-1990
APPLICATION NUMBER: 554,745
FILING DATE: 16-UL-1990
APPLICATION NUMBER: PCT/US 91/04846
FILING DATE: 16-UL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: 31,895
TELECOMMUNICATION NUMBER: 31,895
TELEPHONE: (908) 298-2902
TELEPHONE: (908) 298-5902
TELEPHONE: (908) 298-5388
INFORMATION FOR SEQ ID NO: 1:
                      E: Schering-Plough Corporation 2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/07923724
Patent No. 5780292
GENERL INFORMATION:
APPLICANT: Nevalainen, Helena K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3475 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleotides
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-
                                                            Kenilworth
: New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
CTHER INFORMATION:
US-07-960-389-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                              07033
                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-923-724-7
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1049 CTGAAGGATCCTCGTGCCCAGCGGGCCAATCGTCGCCCAAGATCGACGTGGTCATTTCC 1108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.8%; Score 34.4; DB 2; Length 2363;
48.0%; Pred. No. 1.3;
tive 0; Mismatches 106; Indels 0
SCFUMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
                                                                                                                               PULGASIFICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION NUMBER: US 07/44,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTONNEY/AGENT INFORMATION:
NAME: CIMBAIA, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0240004
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APPLICANT: PALCHEIMO, MARJA T.
APPLICANT: FAGERSTROM, RICHARD B.
APPLICANT: MIETTINEN-OINONEN, ARJA S.
APPLICANT: TURUNEN, MARJA K.
APPLICANT: TURUNEN, MARJA K.
APPLICANT: PIDDINGTON, CHRISTOPHER S.
APPLICANT: PIDDINGTON, CHRISTINE S.
APPLICANT: CANTRELL, MICHAEL A.
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
TITLE OF INVENTION: WELLYMES IN DESIRED RATIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1005 GCCTCCAGCCGCGTAATCGCTCCGCGAAAATTCATTGAGGGCTTCCAGAGCACCAAG 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PELLING DATE: 24-MAY-1995
CLASSIFICATION NUMBER: US/08/374,652C
FILING DATE: 24-MAY-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-UUL-1993
CLASSIFICATION NUMBER: US 07/925,401
FILING DATE: 31-UUL-1992
CLASSIFICATION NUMBER: US 07/925,401
FILING DATE: 31-UUL-1992
CLASSIFICATION NUMBER: 435
ATORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41.264
REGISTRATION NUMBER: 41.264
REGISTRATION NUMBER: 1050.071001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1050.071001
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                                                                                                                                                                                                             NEVALAINEN, HELENA K.M.
  1169 GAATTGGCCGATACCGTCGAAGCC 1192
                                                                                                                               sequence 1, Application US/08374652C
patent No. 5834286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2379 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.85
Best Local Similarity 48.05
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WASHINGTON
                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: NEVALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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LOCATION:
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                                                                             RESULT 8
US-08-374-652C-1
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CITY: WA
STATE: D
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                         APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m. Richard B.
APPLICANT: Houston, Christine S.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FOLKH:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PAPELICATION DATA:
APPLICATION NUMBER: US/08/609,426A
FILING DATE: 01-MAR-1996
CLASSIFICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAMME: Reed, Grant E.
REGISTRATION NUMBER: 1050.0080001
TELEPHONE: (202) 371-2500
TELEFRAX: (202) 371-2500
TENGTHER SEQUENCE CHRARATENCE:
TERMATION FOR SEQUENCE CHRARACTERISTICS:
TENGTHONE: (202) 371-2500
                                                                                                                                                                                                                                         E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
join(404..447, 550..1906)
Piddington, Christopher
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STRANDEDNESS: single
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY;
; LOCATION:
US-08-609-426A-7
                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 1
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Gaps

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42; Indels

Mismatches

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Conservative

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829 acaaatacgagggatggccagagctgctggagatggaggctgcatgccccggaagccat 888
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       Matches
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                                   1065 CTGAAGGATCCTCGTGCCCAGCCGGCCAATCGTCGCCCAAGATCGACGTGGTCATTTCC 1124
                                                                                            312 atgaaaaccatccgtctgccacgctggcttggctcgcccaccaaggagatccaggttaaa 371
                                                                    372 aagtacaagtgtggcctcatcaagccctgcccagccaactactttgcgtttaaaatctgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,189
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/COCKET NUMBER: 26,742
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 201 487-5800
                                                                                                                                                                                                                                                                                                                    APPLICANT: Fischetti, Vincent A.
APPLICANT: Rakonjac, Jasna
APPLICANT: Robbins, John
TITLE OF INVENTION: GENE SERUM OPACITY FACTOR
WOMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      ....OKESSEE: Klauber & Jackson STREET: All Hackensack Avenue CITY: Hackensack STATE: New Jersey COUNTRY: USA ZIP: 07601
                                                                                                                                                                           1185 GAATTGGCCGATACCGTCGAAGCC 1208
                                                                                                                                          432 agtggggccgccaacgtcgtgggc 455
                                                                                                                                                                                                                                                                    Sequence 2, Application US/08294189 Patent No. 5707822 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUCULOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE: NO
FRATURE: -35 sine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
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STRANDEDNESS: double
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57..62
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113..3190
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104..108
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Best Local Similarity
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LOCATION:
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US-08-294-189-2
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DB 2; Length 3240;

Score 33.8; DI Pred. No. 2.3;

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                                                                                                                                                                                                      APPLICANT: ADACHI, HIDEKI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: INOUE, KEIZO
APPLICANT: AND ENION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME
TITLE OF INVENTION: AND GENE THEREOF
TUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEGSTADY, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,917
FILING DATE: 03-40G-1994
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 20943/1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5849557man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 2292-030-0
889 tttagggtggctgtggctcttcctcagccaggggcctgaag 929
                                       463 TITCGCGTCACTATCACTAGAACTAGAAGAGGTCACAGTAG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
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Pred. No. 2.1;
0; Mismatches
                                                                                                                                           Sequence 8, Application US/08283917; Patent No. 5849557; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 248855 OPAT UR
INPORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
ERNGTH: 2085 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.8%;
Best Local Similarity 56.2%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
844..2073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
                                                                                                                        US-08-283-917-8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-08-283-917-8
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312 atgaaaaccatccgtctgccacgctggcctggcctcgcccaccaaggagatccaggttaaa 371
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45.3%; Pred. No. 2.6;
tive 0; Mismatches 145; Indels
52 GGCCTGTCCCCCCTCCTCCGTGTCTCTCACTCAACGCCCGTCGCGGCCGC 1
                                                                                                                                                                                                                                                               Cloning and Expression of Microbial Phytase: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Aspergillus ficuum (Aspergillus niger); STRAIN: NRRL 3135
US-08-151-574-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29,959
FR: 24615-20026.00
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
                                                                                                                                              APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/151,574 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/688,578
FILING DATE: 24 MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MALSAHIGE, KALE H.
NEALSTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                            Sequence 33, Application US/08151574 Patent No. 5436156 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CLC TITLE OF INVENTION: Phy NUMBER OF SEQUENCES: 55 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                     CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94025-3471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic STRANDEDNESS:
                                                            RESULT 12
US-08-151-574-33
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                        122 cacctgctggaccacctcgccttctccatcgaagcagggaagtgggagcctc 173
                                              52 GGCCTGTCCCCCCTCCTCCTCTCACTCAACGCCCGTCGCGGCGC 1
                                                                                                                                                49; Indels
                                                                                                                                                                                                                                                                                                                                                                   3: OBLON, SPIVAK, MCCLELLAND, MAIER & S: NEUSTADT, P.C. 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33.6; DB 3;
Pred. No. 2.1;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
PRICATION NUMBER: US 08/283,917
FILING DATE: 03-AUG-1994
APPLICATION NUMBER: JP 209943/1993
FILING DATE: 03-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5880272man F.
REGISTRATION NUMBER: 2292-030-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 413-2300
TELEFAX: (703) 413-220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
844..2073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-961-716-8
                                                                                                                    RESULT 11
US-08-961-716-8/c
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STREET:

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Query Match

Matches

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372 aagtacaagtgtggcctcatcaagccctgcccagccaactactttgcgtttaaaatctgc 431
                                                                                                                                                492 cctgtgaaaaacaatgtgggcagag 516
                                                                                                                                                                                 724 CGTCTGGAGAACGACCTGTCCGGTG 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: MORRISON & FOERSTER
755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; COCATION: Signal Sequence; LOCATION: 1...72 ); OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZAF: 3**.COMPUTER EARDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1...1401
OTHER INFORMATION:
NAME/KEY: mat_peptide
LOCATION: 70...1401
OTHER INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 755 FOURTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA
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                                                                                                                                                                                                                                       RESULT 14
US-08-693-709-1
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432 agigggccgccaacgicgiggccctactaigtgcittgaagaccgcaigaicaigagi 491
                                  664 GAATIGGCCGATACCGICGAAGCCAATIICACCGCCACGIICGICCCCICCAIICGICAA 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 gocotcatotttgocatagtcacgacatggatgtttattcgaagotacatgagottcagc 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WAN OOIJEN, ALBERT J. J.
APPLICANT: RETVELD, KRIJN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: PEN, JAN
APPLICANT: PEN, JAN
APPLICANT: VERWOERD, TEUNIS C.
APPLICANT: THE EXPRESSION OF PHYTASE IN PLANTS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON : THE STREES
STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: 05/08/146,424
FILING DATE: 02-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44615-20011.24
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Pred. No.
                                                                     492 cctgtgaaaaacaatgtgggcagag 516
                                                                                                      724 CGTCTGGAGAACGACCTGTCCGGTG 748
                                                                                                                                                                                           Sequence 19, Application US/08146424
Patent No. 5593963
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              3: MORRISON & FOERSTER 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INPORMATION:
NAME: KENNEDY, BILL
REGISTRATION UNDHERE: 4461:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 813-5600
TELEFRAX: (415) 494-0792
TELERX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 706141
INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 1404 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.74
Best Local Similarity 45.39
Matches 120; Conservative
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70
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CITY: Palo Alto
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                           RESULT 13
US-08-146-424-19
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US-08-146-424-19
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432 agtggggccgccaacgtcgtgggccctactatgtgctttgaagaccgcatgatcatgagt 491
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                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08693709
Patent No. 5770413
GENERAL INFORMATION:
APPLICANT: VAN OOLJEN, ALBERT J.J.
APPLICANT: RIETVELD, KRIJN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: BEN, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWORED, TEUNIS C.
TITLE OF INVENTION: IN PLANTS
TITLE OF INVENTION: IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,709
FILING DATE: 07-AUG-1996
CLASSIPTCATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/146,424
FILING DATE: 07-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MUTSAHIGE, Kate H
REGISTRATION NUMBER: 29,959
RECISTRATION NUMBER: 29,959
TELECHONE: 415-413-5600
TELEFAX: 415-494-0792
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                                                                                                                                                                                                                                                                                                                                                                               372 aagtacaagtgtggcctcatcaagccctgcccagccaactactttgcgtttaaaatctgc 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 agtggggccgccaacgtcgtgggccctactatgtgctttgaagaccgcatgatcatgagt 491
                                                                                                                                                                    252 geceteatetttgecatagteaegaeatggatgtttattegaagetaeatgagetteage 311
                                                                                                                                                                                                                                            484 GECTCCAGCCGCGTGATCGCCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGCACCAAG 543
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 664 GAATIGGCCGATACCGICGAAGCCAATITCACCGCCACGIICGICCCCICCAIICGICAA
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    Length 1404;
Score 33; DB 2; Length 140.
Pred. No. 2.6;
0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZONDITION OF THE STATE OF 
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,448
FILING DATE: 10-ARR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-08-419-448-33
Sequence 33, Application US/08419448
Patent No. 5863533
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 cctgtgaaaaacaatgtgggcagag 516
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NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 24.
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 33:
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MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
    Query Match 2.7%;
Best Local Similarity 45.3%;
Matches 120; Conservative
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TYPE: nucleic acid
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; ORGANISM: Aspergillus ficuum (Aspergillus niger); STRAIN: NRRL 3135
US-08-419-448-33
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Pred. No. 2.6;
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Best Local Similarity 45.3%;
Matches 120; Conservative
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Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Perfect score:
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SUMMARIES

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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:

Possible reversed clone: polyT not found Seq primer: -40UP from Gibco High quality sequence stop: 403.

Location/Qualifiers
1. 645

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www-bio.llni.gov/bbrp/image/image.html

	FEATURES	BASE COUNT ORIGIN	Query Ma Best Loc Matches	QY 576 Db 645	QY 636 Db 585 Ov 696			Db 405
xk05g02 wu27e06 wf22c03 wo61h03 np76c04 qk45b04	qp56d09 nk14e01 t091c13 mq56b03 wu28c10 of01b11 np21f04 we21e07 mu35b01 wu45d09 nl961e111	AA51424 nfolell.s AA643616 nq79b08.s A1673534 we75b10.x AA543029 nf92e04.s A1821215 ne12h10.v	AA025434 Ze84f10.s AA297147 EST112731 AA470683 nel2h10.s AT733198 nel2h10.s	A1582013 argabo0.x AA297176 EST112740 AA298484 EST114112 A1749731 at32a08.x				EST 18-JAN-2000 s CDNA clone IMAGE:2665874 3' EIN EF-7 ;, mRNA sequence.
- !	498 45 A1348065 594 35 A1348065 508 60 A1801582 479 63 AM012120 464 39 AA622120 464 39 AA622570 455 49 AI660557 530 64 AW050790 417 35 AA582787 443 63 AW0500826 396 36 AA643708 375 51 A1732367	35 35 61	31 34 51	31 31 51	33 33 62 62	34 34 34 34 34	ALIGNMENTS	645 bp mRNA EST NCI_CGAP_CO19 HOMO Sapiens CDNA C SW:EF07_MOUSE P97805 PROTEIN EF-7 GI:6710447
	4 996 8 40.8 495.4 40.6 471.6 38.6 464.3 38.6 474.9 4 36.8 479.4 36.8 479.4 36.8 470.3 32.9 371.4 30.4 370 30.3							1
•	22210000000000000000000000000000000000		C C C 310					RESULT 1 AW300770/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE OCHANTEM

/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/clone=lib="NGI_CGAP_CO19"
/tissue_type="moderately differentiated adenocarcinoma"
/tab.host="inH108"
/note="Organ: colon; Vector: pcWV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Normalized to Cot 50, Average insert size 1.32kb.
Normalized version of NCI_CGAP_CO18. Library constructed
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 645)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Homo sapiens human.

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL COMMENT

Tunor Gene Index Unpublished (1997) On Jul 8, 1999 this sequence version replaced g1:5420873. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov

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Homo sapiens
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1 (bases 1 to 668)

NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

L Unpublished (1997)

On May 9, 1996 this sequence version replaced gi:1132811.

Confact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40UP from Gibco.
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/doganism="Homo sapiens"
/do_xref="taxon:9606"
/clone="IMAGE:2521282"
/clone="IMAGE:2521282"
/tissue=_type="colonic mucosa from 3 patients with Crohn's disease"
                                                                                                                                                                                             AW001287 668 bp mRNA EST 27-OCT-1999 wu27e06.11 Soars_lieckgraefe_colon_NHCD Homo sapiens CONA clone IMAGE: 2521282 3' similar to SW:EF07_MOUSE P97805 PROTEIN EF-7 contains MSR1.t2 MER22 repetitive element ;, mRNA sequence.
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Best Local Similarity 96.89
Matches 639; Conservative
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Tab_host-"DH10B (phage-resistant)"
hote="Organ: colon; Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wf22c03.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone
IMAGE:2351332 3' similar to SW:EF07_MOUSE P97805 PROTEIN EF-7 ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 615)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1134301.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 893 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/dr xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:2351332"
/clone_lib="Soares_Dieckgraefe_colon_NHUC"
/tissue_type="colonic mucosa from 5 ulcerative colitis
                                                                                                                                                                                                                                                                                                                                                                            1101 ttctggaaccagctgtctgtggagagaatggggtgtttcgtcagggactgctgacggt 1160
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gcctgaagaagctcctgcctgac-ttaggagtcagagcccggcaggggctgaggagg
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High quality sequence stop: 476.
Location/Qualifiers
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A1691072
A1691072.1 GI:4902374
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       Quble-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Tissue samples provided by Dr. Brian Dieckgraefe (Washington University, dieck@im.wustl.edu); colonic mucosa represents a range of ulceration, tibrosis, and degeneration. Library constructed by Bento Soares and M. Fatima Bonaldo. "

a 184 c 158 g 149 t 2 others
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wo61h03.xl NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2459861 3'
similar to SW:EF07_MOUSE P97805 PROTEIN EF-7;, mRNA sequence.
A1936111
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                                                                                                                                                                                                                                                                                                          aacaactgggcttccgggacagctgggtcttcataggagccaaagacctcaggggtaaaa
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                                                                                                                                                                   DB 50; Length 615;
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                                                                                                                                                                 48.8%; Score 595.6; DB 50.
llarity 98.2%; Pred. No. 3.6e-152;
Conservative 0; Mismatches 11;
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Homo sapiens

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Notional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

I unpublished (1997)
On May 18, 1998 this sequence version replaced gi:3138334.
Contact: Robert Strausberg* Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg* Rich gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Prayade Dy: Greg Leonnon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: prostate; Vector: p1773D-Pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I: -oligo(dI) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p1773 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
188 c 163 g 161 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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1 (bases 1 to 646)
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illarity 92.8%; Pred. No. 9.9e-145;
Conservative 0; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="normal prostate"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:2459861"
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High quality sequence stop: 438.
Location/Qualiflers
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Gaps

782 446 842 386 902 326 962 266

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Fissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R., Emmert-Buck, M.D., Ph.D. con Library Preparation: M. Bento Soares, Ph.D. con Library Arrayed by: Greg Lennon, Ph.D. con Requencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
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A1245950.1 GI:3841347
EST.
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1 (bases I to 538)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
NAtional Canger Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
On Jan 19, 1998 this sequence version replaced gi:2152876.
On Jan 19, 1998 this sequence version replaced gi:2152876.
Tel:/(301) 496-1550
Emfil: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caggggctgaggaggaggaggaggggtgctgcgtggaaggtgctgcaggtccttgcacg 1022
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                                                                                                                  564 GATCCAGGGACCAAATGTAACGATGAAAGCAGGAAACTCTTCTCTGACTT-GGGAGTTCC
                                                                                                                                                                       723 tacgcaaaacaactgggcttccgggacagctgggtcttcataggagccaaagacctcagg
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                   Length 564
                                                           Indels
                     Score 538; DB 36;
Pred. No. 1.9e-136;
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                   Best Local Similarity (8.9%)
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Ph.D., Ph.D., Ph.D., CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CLone distribution: NI-GAP clone distribution information can be found through the I.M.A.G.E., Consortium/ILNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note--Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. This library is the normalized version of NUI_CGAP_BRI.1. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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                                   285 TGCCTGACTTAGGAGTCAAAGCCCGGCAGGGGCTGAGGAGGAGGAACAAGGGGTGCTGCG 226
                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-1997
IMAGE: 1132230
                                                                                                                                                                                                                                                                                                                                                                                                                  np76c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1132230 similar to TR:G452270 G452270 2-19 PROTEIN PRECURSOR.;, mRNA
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Location/Qualifiers
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/clone_lib="NCI_GGAP_BT2"
/sex="female, pooled"
/tissue_type="breast"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Matches 518; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             44; Length 538;
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I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                        Score 522.2; DB 44
Pred. No. 3.8e-132;
0; Mismatches 3;
                                                                                                                               /db_xref="taxon:9606"
/clone="THAGE:1871887"
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/lab_host="DH108"
               www-bio.llnl.gov/bbrp/image/image.htm]
                                           Std Error: 0.00
                                                                                                                   /organism="Homo sapiens"
                                          Insert Length: 1251 Std Error:
Seq primer: -400P from Gibco
High quallity sequence stop: 479.
Location/Qualifiers
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Best Local Similarity 99.4%;
Matches 524; Conservative (
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Tumor Gene Index

Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1290555.

Contact: Nobert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 518) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seg primer: -40ml3 fwd, ET from Amersham
High quality sequence stop: 452.
Location/Qualifiers
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ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS

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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anote—"Organ: colon; Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I coligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaido. "

154 c 131 g 115 t
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                                                                                                                                                                                                                                                                                                            AI348065 498 bp mRNA EST 02-FEB-1999 qp56d09.xl NCI_CGAP_CO8 Homo sapiens cDNA clone IMAGE:1927025 3's similar to TR:P97805 P97805 EF-7;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 498) NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
1032 gcctctcctcctcggaaacagaaccctcccacagcacatcctacccggaagaccagcctc 1091
                                                                               1092 agagggtccttctggaaccagctgtctgtggagagaatggggtgctttcgtcagggactg 1151
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                                                                                                     Tumor Gene Index
Unpublished (1997)
On Peb 6, 1998 this sequence version replaced gi:2848226.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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/db_xref="taxon:9606"
/clone="IMAGE:1927025"
/clone_lib="NOI_CGAP_CO8"
/tissue_type="adenocarcinoma"
/lab_host="bH108"
                                                                                                                                                                                         CTGACGCTGGTCCTGAGGAAGGACAAACTGCCCAGAC 1
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High quality sequence stop: 459.
Location/Qualifiers
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AI348065/c
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 594)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                             963 caggggctgaggaggaggagcagggggtgctgcgtggaaggtgctgcaggtccttgcacg 1022
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318 GCCTCTTCCTCAGCCAGGGCCCTGAAGAACTCCTGCCTGACTTAGGAGTCAGAGCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 ACCAGCCTCAGAGGTCCTTCTGGAACCAGCTGTCTGTGGGGGAAAGGGGTGCTTTCGT
                                                                                              tggccagagctgctggagatggagggctgcatgcccccgaagccattttagggtggctgt
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Unpublished (1997)
On Nov. 29, 1993 this sequence version replaced gi:502047.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg(aih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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High quality sequence stop: 347.
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          /clone_lib="NCI_CGAP_Co2"
/tissue_type="tumor"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: colon; Vector: Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Bulk colon villous adenoma. 5' adaptor sequence:
5' GAATTGGCACGACGAC 3' 3' adaptor sequence: 5'
CCGACTTTTTTTTTTTTTTT 3' Average insert size: 1.1 kb."
175 c 154 g 140 t
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Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 508)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                            534 GGGAAACTCTCTCGTGACCGGGGAAGCTCCTACGCAAAACAATTGGGCTTCCGGACCAGC 475
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                                                                                                                                                                                                                                                        ggtgcactggtgctggtggcctcctacgacgatccagggaccaaaatgaacgatgaaagc 692
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                                                                                                                                                                                         Score 496.8; DB 35; Length
Pred. No. 3.4e-125;
0; Mismatches 27; Indels
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Best Local Similarity 94.7%;
Matches 557; Conservative (
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TITLE
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cond. Library Preparation: Life Technologies, Inc.

cond. Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-GGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/clone="liMAGE:2185652"
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/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH108"
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On Mar 10, 1998 this sequence version replaced g1:2948662
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.6%; Score 495.4; DB 60; Length 508; 99.6%; Pred. No. 7.7e-125; 1ve 0; Mismatches 1; Indels 1;
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                                                            Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                          Seg primer: -400P from Glbco
High quality sequence stop: 352.
Location/Qualiflers
1. .508
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1073

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:2521362"
/clone="lib="Soares_Dieckgraefe_colon_NHCD"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 479)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Onpublished (1997)
On May 9, 1996 this sequence version replaced gi:1132845.
On May 9, 1996 this sequence version replaced gi:1132845.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 966-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Giboo.
Location/Qualifiers
                                                                                                                                                                                                                                                                                          954 agagcccggcagggctgaggaggaggagcaggggtgctgcgtggaaggtgctgcaggt 1013
/lab_host="DH10B (phage-resistant)"
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AW001308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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                                                                                           AA622120 518 bp mRNA EST 14-OCT-1997 nq56b03.s1 NCI_CGAP_CO9 Homo sapiens cDNA clone IMAGE:1147853 3' similar to TR:G452270 G452270 2-19 PROTEIN PRECURSOR. ;, mRNA
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 518)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Uppublished (1997)
Uppublished (1997)
Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert, Strausbergenih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٦;
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Pred. No. 1e-124;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seg primer: -40ml3 fwd. ET from Amersham
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     29 TIGAGCCCAATTAAATTITATTITGCIG 1
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99.8%;
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 461)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclcgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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100.0%; Pred. No. 2.8e-116;
tive 0; Mismatches 0;
                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
          ity sequence stop: 453.
Location/Qualifiers
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          High quality
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In Onpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2153278.
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Email: Robert_Strausberg@nih.gov
Tal: (301) 466-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Preparation: Stratagene, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 464)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
NCI-CGAP trop://www.ncbi.nlm.nih.gov/nciogap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1030 gegeeteteeteeteggaaacagaaceeteecacagacacateetaceeggaagaccagec 1089
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                                                                                                                                                                                                       aacaactgggcttccgggacagctgggtcttcataggagccaaagacctcaggggtaaaa 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA847242 464 bp mRNA EST 31-MAR-1998 of01b11.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1419837 similar to TR:P97805 P97805 EF-7; , mRNA sequence,
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                      63; Length 479;
                                                                                                                                                         Indels
                                                                                                   Score 471.6; DB 63
Pred. No. 2.4e-118;
0; Mismatches 4;
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Seq primer: -40ml3 fwd. ET from Amersham
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  125
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AA847242.1 GI:2933760
                                                                                                   38.68;
99.28;
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                                                                                                                      Best Local Similarity 99.2
Matches 474; Conservative
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93
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AA847242/c DEFINITION

RESULT

ACCESSION

VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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45

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Gaps

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Length 464; Indels 845

345

JOURNAL

FEATURES

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AA552362.1 GI:2322614
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Best Local Similarity 99.8%;
Matches 450; Conservative
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ORIGIN
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             DEFINITION
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TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                              on Sep 29, 1997 this sequence version replaced gi:1520561.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550.

Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaacaactgggcttccgggacagctgggtcttcataggagccaaagacctcaggggtaaa 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461 AAACAACTGGCTTTCCGTGACAGCTGGGTCTTCATAGGAGCCAAAGACCTCAGGGGTAAA 402
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Pred. No. 3.8e-114;
0; Mismatches 3;
                                                                                                                                                                                              Insert Length: 681 Std Error: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 381.
Location/Qualifiers
                                                                                                                                                                   www-bio.llnī.gov/bbrp/image/image.html
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Unpublished (1997)
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Matches 729 789

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Sequencing Center information can be
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332
AA552362 454 bp mRNA EST 05-SEP-1997 nk04h09.s1 NCI_CGAP_CO2 Homo sapiens cDNA clone IMAGE:1012577 similar to TR:G452270 G452270 2-19 PROTEIN PRECURSOR. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Emall: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert_Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 449.4; DB 35,
Pred. No. 2.7e-112;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Arraying: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 1355 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 446.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ww-bio.llni.gov/bbrp/image/image.html
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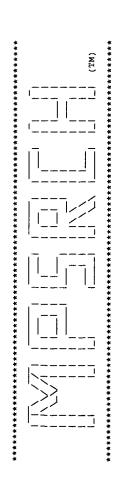
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1089

RESULT 15 AA552362/c

1128 atggggtgctttcgtcagggactgctgacggctgtcctgaggaagga
1128 atggggtgctttcgtc
112

Search completed: May 31, 2000, 17:51:15 Job time: 3432 sec



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed May 31 11:04:55 2000; MasPar time 21.50 Seconds 719.210 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-186-342-2 (1-223) from US09186342.pep 1686 1 MRVSGVLRLLALIFAIVTIW......KYEGWPELLEMEGCMPRPF 223 Description: Perfect Score: Sequence:

Scoring table:

Searched:

PAM 150 Gap 11

225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb112

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 45.504; Variance 84.613; scale 0.538 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ					
Result No.	Score	Query	Query Match Length DB	BB	A	Description	Pred. No.
T	110	6.5	44	11	088417	HYPOTHETICAL 5.0 KD PR	2.54e-02
7	110	6.5	3190	S	001368	CREB-BINDING PROTEIN H	2.54e-02
ო	108	6.4	1001	S	094526	TWO P DOMAIN POTASSIUM	4.90e-02
4	103	6.1	358	S	045691	MO1E5.2 PROTEIN.	2.44e - 01
2	101	9.0	253	Н	029937	HYPOTHETICAL 30.2 KD P	4.58e-01
9	102	9.0	2285	Ŋ	077292	KAKAPO (FRAGMENT).	3.35e-01
7	102	9.0	2396	Ŋ	07.7291	KAKAPO (FRAGMENT).	3.35e-01
æ	100	5.9	510	Ŋ	096387	INOSINE-5'-MONOPHOSPHA	6.25e-01
φ	66	5.9	531	9	Q9XS55	UDP-GLUCURONOSYLTRANSF	8.52e-01
10	66	8.9	532	9	09xs56	UDP-GLUCURONOSYLTRANSF	8.52e-01
11	96	5.8	386	7	082844	XYLOSE REPRESSOR.	1.16e+00
12	97	5.8	366	1	Q921K1	HS1 BINDING PROTEIN 3.	1.57e+00
13	97	5.8	561	7	052072	PHA SYNTHASE.	1.57e+00
14	97	5.8	1134	٦	030078	MOLYBDOPTERIN OXIDORED	1.57e+00
15	96	5.7	269	S	018188	COSMID C25H3,	2.12e+00
16	96	5.7	320	S	018887	SIMILARITY TO FREQUENI	2.12e+00
17	96	5.7	389	10	080586	PUTATIVE N-MYRISTOYLTR	2.12e+00
18	95	5.6	124	7	086225	HYPOTHETICAL 14.5 KD P	2.87e+00
19	95	5.6	233	٣	012131	N-(5'-PHOSPHORIBOSYL)-	2.87e+00
20	94	5.6	240	~	051829	INNER MEMBRANE PROTEIN	3.86e+00

COIH6.6 PROTEIN. SIMILAR TO GAMMA-GLUTA 3 CHLI PROTEIN (FRAGMENT 3 RETINOBLASTOMA-ASSOCIA 3	HELICASE. 3. CHLI POTENTIAL HELICAS 3. F46F6.2 PROTEIN. 2. BACTERIOPHAGE-LIKE GEN 6. C13D9.5 PROTEIN.	BUZIZ.4 PROTEIN. FIBEZ.4 PROTEIN. 6. HYPOTHETICAL 54.8 KD P 5. SIMILAR TO FRUCTOSE-2. 6. UDP-GLUCURONOSXLTRANSF 5.	04649 UDP-GLUCURONOSYLTRANSF 5.18e+00 03499 YVRG PROTEIN. 5.18e+00 03499 YVRG PROTEIN. 6.95e+00 081909 T7123.15 PROTEIN. 6.95e+00 097AF9 257AA LONG HYPOTHETICA 9.28e+00 093719 F4369.7 PROTEIN. 9.28e+00	18 COLLAGENASE PRECURSOR. 9. 58 SIL. 72 PUTATIVE OXIDOREDUCTAS 1. 94 ASPARTATE AMINOTRANSFE 1.
350 547 556 642	906 906 1018 178 291		533 573 805 1865 1 257 805	1282 1287 388 463 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GGMQQVVGTQMGMVNSMPMS-ISNNGNNGMNAIPGMNTIAQGNLGNMVLTNSVGGGMGGM 239
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                 AKIMARU H., CHEN Y., DAI P., HOU D.X., NONAKA M., SMOLIK S.M., ARMSTRONG S., GOODMAN R.H., ISHII S.; "Drosophila CBP is a co-activator of cubitus interruptus in hedgehog
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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9
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                                                                                                                                                                                                                                                                                                                                 Query Match 6.5%; Score 110; DB 5; Length 3190; Best Local Similarity 33.8%; Pred. No. 2.54e-02; Matches 24; Conservative 14; Mismatches 30; Trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 108; DB 5; Length 1001; Pred. No. 4.90e-02;
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TISSUB-BRAIN AND MUSCLES OF ADULTS;
GOLDSTEIN S.A.N., PRICE L.A., ROSENTHAL D.N., PAUSCH M.H.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, U55321; AAC69250.1;
FLYBASE; FBgn0017561; Ork1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAUSCH M.H.;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1001 AA; 109290 MW; A57C4B04 CRC32;
                                                                                                                                                                                                                                                                                               3190 AA; 331879 MW; A44A25BF CRC32;
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01-MAY-1999 (TrEMBLrel. 10, Last and
TWO P DOMAIN POTASSIUM CHANNEL ORKI
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TISSUE-BRAIN AND MUSCLES OF ADULTS;
MEDLINE; 97075152,
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TISSUE-BRAIN AND MUSCLES OF ADULTS;
                                                                                         signaliing.";
Nature 386:735-738(1997).
EMBL; U88570; AAB53050.1; -.
FLYBASE; FBG00015624; nej.
PFAM; PF00439; bromodomain; 1.
PFAM; PF00569; Zz; 1.
                                                                                                                                                                                                                                                                      PRINTS; PR00503; BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, 01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.48;
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Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 VNHLKQQPGGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 VKFLKEIPGGA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ionic channel
SEQUENCE 10
                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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셤
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RESULT

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STRAIN-VC-16 / DSM 4304 / ATCC 49558;
STRAIN-VC-16 / DSM 4304 / ATCC 49558;
STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE; 98049343.
KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RICHARDSON D.L., KERLANAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.
KIKKNESS E.F., DOGHERYY B.A., MCKENNEY K., ADAMS M.D., LOFFUYS B.,
PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
OVERBEEK R., GOGAYNEN J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
COTTON M.D., SPRIGGS T., BATTACH P., KAINE B.P., SYKES S.M.,
SADOW P.M., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 94150718

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A., BOUTON D., CONNELL M., CONSET Y., COOPER J., COULSON A., ENATELL D., LOTHELL D., TO COPER J., COULSON A., GRANDIREL D., BURTON D., CONSET J., LOTHON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JOHNSTON B., KIRSTEN J., LAISTER N., LATERILLE P., LIGHTNING J., LLOYD C., KIRSTEN J., LAISTER N., LATERILLE P., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SAUNDERS D., SHOWNKEEN R., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WALTSKON J., WALKINSON S., WALLDAN S., WATERSTON R., WALKINSON S., WALLDAN P.; TO OOR CONTIGUOUS NUCLEOCITIES SEQUENCE from Chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 ISFLKHIERCESLWYVLDYS-TGS-LTDQYKMLRVELEG-YQKGLGDRASTIVINKIDLS 314
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 6.1%; Score 103; DB 5; Length 358; Best Local Similarity 37.3%; Pred. No. 2.44e-01; Matches 25; Conservative 11; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                       Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 293385; CAB07637.1; -.
PFAM; PF01018; GTP1_0BG; 1.
PRINTS; PR00326; GTP10BG.
SEQUENCE 358 AA; 39356 MW; E44EC56B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seq
01-AUG-1998 (TrEMBLrel. 07, Last anno
                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                       01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                               MOIES.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 GKSPEEE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 GKSPFEQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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045691;
                                                                                                                                                                                                                                                                                                                     DOBSON
                                                                                                                                             M01E5.
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1020 QFLAMGPE 1027
                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 QFLKNSPD 201
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                                                                                                                                                                                                                                                                                                               NON_TER
SEQUENCE
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Q9XS55
Q9XS55;
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096387
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TISSUE-EMBRYONIC AND IMAGINAL DISC;
GREGORY S.L., BROWN N.H.;
"Rakapo, a Gene Required for Adhesion Between and Within Cell Layers
in Drosophila, Encodes a Large Cytoskeletal Linker Protein Related to
Plectin and Dystrophin.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ011925; CAR09870.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Perrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  851 IPGACLLLPPP-DQEAIDAAERLKRLFDRSVALWQKKHLRLRQNMIFATIRVVKG-WDFD 908
                                                                                                                                                                                                                                                                                             190 EYFPEFKASVIRTNVQFSPDMPLEERLKI--IKNEVGKDFYKKLMEINEEDMVLWEKVVD 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                               Gaps
                 "The complete genome sequence of the hyperthermophilic, sulphatereducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL; AE001083; AAB90927.1; -.
HYGR; AE0307; -.
Hypothetical protein.
SEQUENCE 253 AA; 30215 MW; EE14DFE4 CRC32;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 102, DB 5; Length 2285;
Pred. No. 3.35e-01;
22; Mismatches 25; Indels
                                                                                                                                                                                 Score 101; DB 1; Length 253;
Pred. No. 4.58e-01;
15; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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PFAM; PF00307; CH; 2.
PFAM; PF00018; SH3; 1.
PFAM; PF00435; spectrin; 15.
NON_TER 2285 2285
SEQUENCE 2285 AA; 262579 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 08, (TrEMBLrel. 08, (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.0%;
Best Local Similarity 26.5%;
Matches 18; Conservative
                                                                                                                                                                                     Query Match 6.0%;
Best Local Similarity 33.9%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998
01-NOV-1999
  VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                             248 MY 249
                                                                                                                                                                                                                                                                                                                                                                                                     120 MY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 6
077292
077292;
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                                                                                                                    TISSUB-EMBRYONIC AND IMAGINAL DISC;
GREGORY S.L., BROWN N.H.;
GREGORY S.L., BROWN N.H.;
"kakapo, a Gene Required for Adhesion Between and Within Cell Layers
"kakapo, a Gene Required for Adhesion Between and Within Cell Layers
"no Drosophila, Encodes a Large Cytoskeletal Linker Protein Related to
Plectin and Dystrophin.";
Submitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ011924; CAA09869.1; -.
PRAM; PF00307; CH; 2.
PFAM; PF00018; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00018; SP6011; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 VKKYKCGLIKPCPANYFAFKICS-GAANVUGPTMCFEDRMIMSPVKNNVGRGLNIAL-VN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 VMSYTYDVII-CMPGYIDFALSDIDLTNNMTDNITLKTPVISSPMDTVTGHKMSIALALS 72
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 102; DB 5; Length 2396;
Pred. No. 3.35e-01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.9%; Score 100; DB 5; Length 510; Best Local Similarity 21.2%; Pred. No. 6.25e-01; Matches 18; Conservative 26; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE G.L., JAMES A.A., LUECKE H.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF035679; AAD10256.1; -
HSSP; P50097; 1AK5.
PROSITE; PS00487; IMP_DH_GMP_RED; 1.
PROSITE; PS00487; IMP_DH_GMP_RED; 1.
PROSITE; PS00487; IMP_DH_GMP_RED; 1.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2D316313 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    510 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 GTTGAVLGQKAFDMYSGDVMHLVKF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 GGLGVIHNNMSIEKQIEEVKKVKRF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2396 AA; 274955 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UDP-GLUCURONOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.0%;
Best Local Similarity 26.5%;
Matches 18; Conservative
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STRAIN-BALB/C;
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Q9Z1K1
Q9Z1K1;
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052072
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Pred. No. 8.52e-01;
36; Mismatches 43; Indels 10; Gaps 10;
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                                                                                                   KOBAYASHI T., TATANO A., YOKOTA H., ONAGA T., WATANABE T., YUASA A.; "Small intestinal UDP-glucuronosyltransferase shedGTIA07: partial purification and cDNA cloning from sheep small intestine."; Arch. Blochem. Blochys. 364:143-152(1999).
EMBL; AB018477; BAA774751; -.
PROSITE; PS00375; UDPGT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            32 KTIRLPRWLASPTKEIQVKKYKCGLIKPCPANYFAFK-ICSGAANVVGPTMCFEDRMIMS
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EMBL; ABO18478; BAA77456.1; -...
PROSITE; PSO0375; UDPGT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 PVKNNVGRGLNIALVNGTTGAVLGQ-KA-F-DM-YSGDVWHLVKFIKEIPGGALVL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
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                                                                                                                                                                                                                                                                                              Score 99; DB 6; Length 531;
Pred. No. 8.52e-01;
36; Mismatches 43; Indels 10;
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                                                                                                                                                                                                                                                       531 AA; 60823 MW; DC5D6014 CRC32;
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01.00v-1999 (Tremblrel. 08, L

01.00v-1999 (Tremblrel. 12, L
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Local Similarity 23.3%;
les 27; Conservative
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Local Similarity 23.3%;
les 27; Conservative
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                                        FROM N.A.
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                                                                 STRAIN-SAFORK
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  Caprinae;
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Matches
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                                                                                                                                    TAKEDA Y., TAKASE K., YAWATO I., ABE K.;

TAKEDA Y., TAKASE K., YAWATO I., ABE K.;

"Sequencing and characterization of the xyl operon of a gram-positive bacterium, Tetragenococcus halophila.";

Appl. Environ. Microbiol. 64:2513-2519(1998).

EMBL; AB009553; BAA31870.1;

PROSITE; PS01125; RK; 1.

SEQUENCE 386 As; 43426 MW; B2B31CBB CRG32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 EVIQLLKNNAKLISIGVNNIVSMYDPETVVINNELYREIPDLINVIEKHLTRRNNRNVFI 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Tetragenococcus halophilus (Pediococcus halophilus).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
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"Isolation and characterization of a novel HS1 SH3 domain binding protein, HS1BP3.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ132192, CAA10600.1; -.
SEQUENCE 396 AA; 43769 MW; ODCA7DDE CRC32;
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Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Actinomycetales; Corynebacterineae; Nocardiaceae; Nocardia.
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Last annotation update)
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Last annotation update)
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Pred. No. 1.57e+00;
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SEQUENCE FROM N.A.
HALL B., BALDWIN J., RHIE H.G., DENNIS D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                561
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06,
10,
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Local Similarity 32.6%;
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Matches 21; Conservative
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01-MAY-1999 (TrEMBLrel.
HS1 BINDING PROTEIN 3.
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01-JUN-1998 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
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                                                                                               SEQUENCE FROM N.A.
                                                    Tetragenococcus.
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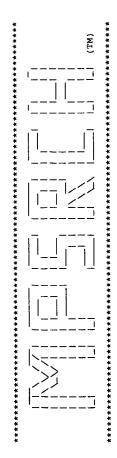
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KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
KICHARDSON D.L., KERLANAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
FLEISCHMANN R.D., QUACKENBUGH D.A., L. LET N.H., SUTTON G.G., GILL S.,
KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFFUCS B.,
PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
OVERBEEK R., GOCANNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
SADOW P.W., D'ANNIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
AMSON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 990 VVAAVEPTVVKGTIAIPVGMGRWADSAVKKPAYFRLNDGSVAALVS---ELPDGA-SLPS 1045
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                                                                                            Gaps
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Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
                                                                                                                      239 VEYSVGRGLQTFLLSWRNPTAEQGDWDFDTYAGRVIRAIDEVREITGSDDVNLIG 293
                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MOLYBDOPTERIN OXIDOREDUCTASE, MOLYBDOPTERIN BINDING SUBUNIT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 97; DB 1; Length 1134;
Pred. No. 1.57e+00;
23; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
                                                                Score 97; DB 2; Length 561;
Pred. No. 1.57e+00;
13; Mismatches 21; Indels
 to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E6FF75AE CRC32;
                                       60406 MW; 7A21B91A CRC32;
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                                                                                                                                                                                                        PRT; 1134 AA.
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN~VC-16 / DSM 4304 / ATCC 49558;
MEDLINE; 98049343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 1134 AA; 127688 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001095; AAB91069.1; -.
                         PFAM; PF00561; abhydrolase;
SEQUENCE 561 AA; 60406 MP
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            EMBL; AF019964; AAB94058.1;
                                                                Query Match 5.8%;
Best Local Similarity 34.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 27.3%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%;
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                                                                                                                                                                                                                                 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                Archaeoglobus fulgidus.
Submitted (AUG-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COSMID C25H3.
                                                                                                                                                                                                                                                                                          PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C25H3.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ir 15
Q18188
Q18188;
                                                                                                                                                                                         LT 14
030078
030078;
                                                                                                                                                                                                                                                                                                      AF0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                          RESULT
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WILESON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERY T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPERY T., COOPER J., COULSON A.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAM J., KIRSTEN J., LASTER N., LATREILLE P.,
SMALDON J., PERCY C., MCMURRAR A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., SOOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 96; DB 5; Length 269;
Pred. No. 2.12e+00;
11; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 NQESRNFYHPLSGDHFRK--FRGDWLEIGQNRLRS-SDISTFLKN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U29535; AAA68788.1; -.
SEQUENCE 269 AA; 31750 MW; 6158031C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%;
nilarity 37.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WATERSTON R.;
Submitted (JUN-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
                                                            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed May 31 11:04:26 2000; MasPar time 8.90 Seconds 762.806 Million cell updates/sec Tabular output not generated.

Run on:

1 MRVSGVLRLLALIFALVTTW....., KYEGWPELLEMEGCMPPKPF 223 >US-09-186-342-2 (1-223) from US09186342.pep 1686 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

83857 seqs, 30454973 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot38 1:swissprot Database:

Mean 47.338; Variance 81.778; scale 0.579 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.14e-179	9.26e-167	3.13e-120	6.70e-02	8.83e-01	8.83e - 01	1.21e+00	1.21e+00	1.21e+00	1.21e+00	3.01e+00	4.07e+00	4.07e+00	4.07e+00	4.07e+00	7.34e+00	5.47e+00	7.34e+00	7.34e+00	5.47e+00	7.34e+00	5.47e+00	5.47e+00
Description	2-19 PROTEIN PRECURSOR	PROTEIN GS3786.	ONCOPROTEIN INDUCED PR	PUTATIVE STEROID DEHYD	56 KD TYPE-SPECIFIC AN	56 KD TYPE-SPECIFIC AN	HYPOTHETICAL PROTEIN H	N-(5'-PHOSPHORIBOSYL)A	N-FORMYL PEPTIDE RECEP	CHITIN SYNTHASE 3 (EC	SOMATOTROPIN PRECURSOR	MITOCHONDRIAL THIOREDO	ANAEROBIC DIMETHYL SUL	HYPOTHETICAL 41.5 KD P	4 - COUMARATE COA LIGAS	ARTA PROTEIN.	HYPOTHETICAL 15.4 KD P	FPLEFT PROTEIN (FRAGME	SOMATOTROPIN PRECURSOR	MOVEMENT PROTEIN (CELL	SHAKING-B PROTEIN PREC	CREATINASE (EC 3.5.3.3	HYPOTHETICAL 47.6 KD P
ΙD	219_HUMAN	G786_HUMAN	OIT1_MOUSE	DHBK_MOUSE	TSAW_RICTS	TSAK_RICTS	Y48A_HAEIN	TRPF_YEAST	FML2_MACMU	CHS3_EXODE	SOMA_TRIVU	THI2_BOVIN	DMSC_ECOLI	YAM3_SCHPO	4CL_ORYSA	ARTA_ECOLI	YMFS_ECOLI	VFPL_FOWP1	SOMA_SEROU	MOVP_TMGMV	SHAK DROME	CREA_BACSP	YMI4_CAEEL
DB	; 1	Н	٦	Н	Н	Н	***	7	٦	Н	Н	П	-	Н	Н	, -	~1	H	П	П	~	Н	Н
Length DB	230	227	115	312	522	532	124	224	349	885	215	166	287	382	563	104	137	159	204	256	361	410	428
% Query Match	53.9	50.7	39.0	6.2	5.7	5.7	5.6	5.6	5.6	5.6	5.5	5.4	5.4	5.4	5.4	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3
Score	806	855	658	104	96	96	95	95	95	95	92	91	91	91	91	83	90	89	8	90	8	06	90
Result No.	1	7	m	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

5.47e+00 5.47e+00	7.34e+00	7.34e+00	9.82e+00	1.31e+01	9.82e+00	1.31e+01	9.82e+00	9.82e+00	9.82e+00	1.31e+01	1.31e+01	1.31e+01	9.82e+00	1.31e+01	1.31e+01	1.31e+01	1.31e+01	1.31e+01	9.82e+00	1.74e+01
NAD(P) TRANSHYDROGENAS 6PF-2-K/FRU-2,6-P2ASE	PUTATIVE CDP-DIACYLGLY	GLYCEROL-3-PHOSPHATE D	MITOCHONDRIAL THIOREDO	PROBABLE 6-PHOSPHO-BET	SOMATOTROPIN PRECURSOR	X INACTIVE SPECIFIC TR	HYPOTHETICAL PROTEIN M	HYPOTHETICAL PROTEIN H	PROBABLE ATP-DEPENDENT	6PF-2-K/FRU-2,6-P2ASE	WD-REPEAT PROTEIN SAZD	HOMEOBOX PROTEIN DTH-1	PUTATIVE TRANSPORTER C	HYPOTHETICAL 70.6 KD P	AMILORIDE-SENSITIVE SO	CYCLOMALTODEXTRIN GLUC	DOLICHYL-PHOSPHATE-MAN	MAJOR VAULT PROTEIN (M	GENOME POLYPROTEIN [CO	ALANYL-TRNA SYNTHETASE
PNTB_ECOLI F263_RAT	PEL1_YEAST	GPDM_YEAST	THIZ_RAT	GLVG_ECOLI	SOMA_SHEEP	XIST_MOUSE	Y381_METJA	Y285_HELPY	DBP8_YEAST	F263_HUMAN	SAZD_HUMAN	HMH1_DUGTI	YE1F_SCHPO	YGC3_YEAST	SCAB_HUMAN	CDGT_BACSP	PMT2_YEAST	MVP_RAT	POLG_MVEV	SYA_THIFE
н н	н.	н,	-	-	Н	1	7	Н	r-4	٦	,	Н	-	-	Н	Н	~	٦	٦	7
462	518	649	166	212	217	298	320	418	431	468	519	533	628	635	640	713	758	882	1780	877
5.3	5.3	5.3	5.2	5.2	5.2	5.3	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.1
06	88	6 8	88	87	88	87	88	88	88	87	87	87	88	87	87	87	87	87	88	98
24	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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LT 3
OIT1_MOUSE
P97805;
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                                                                                                                                                                                                                          61 LPQPCPEEHLAFRVVSGAANVIGPKICLEDKMLMSSVKDNVGRGLNIALVNGVSGELIEA 120
                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YFDMWGGDVAPFIEFLKAIQDGTIVLMGTYDDGATKLNDEARRLIADLGSTSITNLGFRD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKACPEKHFAFKMASGAANVVGPKICLEDNVLMSGVKNNVGRGINVALANGKTGEVLDTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRLAGPLRIVVLVVSVGVTWIVVSILLGGPGSGFPRIQQLFTSPESSVTAAPRARKYKCG 60
                                                                                                                            1 MRVAGAAKLVVAVAVFLLTFYVISQVFEIKMDASLGNLFARSALDTAARSTKPPRYKCGI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Onto I., Hashimoto J., Takaoka K., Ochi T., Okubo K., Matsubara K.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE 2-19 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
                                                                                                                                                                                                              RAFDMWAGDVNDLLKFIRPLHEGTLVFVASYDDPATKMNEETRKLFSELGSRNAKELAFR
                                                                                       .;
2
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                              Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.7%; Score 855; DB 1; Length 227; larity 51.6%; Pred. No. 9.26e-167; Conservative 49; Mismatches 56; Indels
                                                                                       Indels
                                                                                                                                                                                                                                                                             181 DSWVFVGAKGVQNKSPFEQHVKNSKHSNKYEGCPEALEMEGCIPRRS 227
           33 POTENTIAL.
230 2-19 PROTEIN.
25069 MW; FE3934D91F98CAAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D87120; BAA13251.1; -.
SEQUENCE 227 AA; 24680 MW; 6DC94B259052647F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NWVFCGGKGIKTKSPFEQHIKNNKDTNKYEGWPEVVEMEGCIPQK 225
                                                                                      56; Mismatches 45;
                                                             Score 908; DB 1; I
Pred. No. 2.14e-179;
                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
PROFEIN GS3786.
                                                                                                                                                                                                                                                                                                                                        227 AA
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                            / Match 53.9%;
Local Similarity 53.3%;
Nes 121; Conservative
                                                                                                                                                                                                                                                                                                                                        STANDARD;
           1
34 2
230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 116; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-BONE
                                                                                                                                                                                                                                                                                                                                      G786_HUMAN
092520;
                                    SEQUENCE
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                         Best Loca
Matches
                          CHAIN
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--- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY. 17-BETA-HSD 3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGQVMKKDSFDMYSGDPQLLLNFLTEIPDSTLVLVASYDDPGTKMNDKIKTLFSNLGSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AKQLGFRDSWVFVGAKDLKSKSPYEQFLKNNPETNKYDGWPELLELEGCVPRK 113
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                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                    Fu X., Kamps M.P., "E2a-Pbx1 induces aberrant expression of tissue-specific and developmentally regulated genes when expressed in NIH 3T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.0%; Score 65%; DB 1; Length 115;
larity 73.5%; Pred. No. 3.13e-120;
Conservative 17; Mismatches 13; Indels
                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
ONCOPROTEIN INDUCED PROTEIN I (PROTEIN EF-7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 AA; 13022 MW; DDF764E950B4EABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Eutheria, Rodentia, Sclurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Cell. Biol. 17:1503-1512(1997).
-!- SIMILARITY: BELONGS TO THE 2-19 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U72677; AAB51037.1; -.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1201784; OIT1
                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                     MEDLINE; 97184476.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           STRAIN-BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DHBK_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
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Query Match

ST TW BRANKERS

Matches

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532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56785 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M33004; AAA26391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%;
ilarity 30.2%;
Conservative
                                                                                                ANTIGEN) (STA56) (TSK56).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                            Rickettsia tsutsugamushi
            STANDARD;
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Haemophilus influenzae
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364
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480
532 AA;
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                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 YLG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 QLG 173
                                                                                                                                                                                     STRAIN-KARP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y48A_HAEIN
086225;
          TSAK_RICTS
P37915;
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TRANSMEM
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         entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch)
Usage by and for commercial
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                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohashi N., Nashimoto H., Ikeda H., Tamura A.;
"Diversity of immunodominant 56 kDa type-specific antigen (TSA) of Rickettsia tsutsugamushi. Sequence and comparative analyses of the genes encoding TSA homologues from four antigenic variants.";
J. Biol. Chem. 267:12728-12735(1992).
-!- FUNCTION: MAY BE AN ADHERENT FACTOR FOR RICKETTSIAL ADSORPTION TO THE HOST-CELL SURFACE AND A DETERMINANT OF VIRULENCE OF INDIVIDUAL RICKETTSIAL STRAIN. II IS THE MAJOR OUTER MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 VLSDKITQIYS-DIRQFAKIANIEVPGAPLPNSASVEQIQTKMQELN-DVLEELRESF 307
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                             01-00T-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
56 KD TYPE-SPECIFIC ANTIGEN PRECURSOR (TSA) (56 KD SCRUB TYPHUS
                                                                                                                                                                                                     4;
                                       Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Orientia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 8.83e-01;
20; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
56 KD TYPE-SPECIFIC ANTIGEN.
ALA/GLN-RICH.
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                                                                                                                                                                                                                               268 RTTGYVIHSLMGSINSIMPRWMYFKIIMGFS-KSLR-NRYLKKRKKN 312
                                                                                                                                                                                                                                              2 RVSG-VLR-LLALIFALVTTWMFIRSYMSFSMKTIRLPRWLASPTKE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64CB0E3B1B5A2EB6 CRC64;
                                                                                                                                                                       Score 104; DB 1; Pred. No. 6.70e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                  14; Mismatches
                                                                                                                                                                                                                                                                                                                     522 AA.
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; B42804; B42804.
Antigen; Signal; Transmembrane; Virulence.
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                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55971 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M63383; AAA26398.1; -.
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Best Local Similarity 31.0%;
Matches 18; Conservative
                                                                                                                                                                       Match 6.2%;
Local Similarity 34.0%;
les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia tsutsugamushi.
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         ANTIGEN) (STA56) (TSW56)
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324
67
470
522 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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TSAW_RICTS
P37919;
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TRANSMEM TRANSMEM SEQUENCE

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SIGNAL DOMAIN CHAIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNATION NATION OF STATE AND STATE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                 01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01.FEB-1995 (Rel. 31, Last annotation update)
56 KD TYPE-SPECIFIC ANTIGEN PRECURSOR (TSA) (56 KD SCRUB TYPHUS
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Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Orientia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 KD TYPE-SPECIFIC ANTIGEN.
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15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
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SIGNAL 1 22 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                             White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D., Peterson J., Hickey E., Dodson R., Gwinn M.; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tschumper G., Carbon J.; "Sequence of a yeast DNA fragment containing a chromosomal replicator and the TRP1 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M., Weddman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C. Fine L.D., Fritchman J.L., Geoghagen N.S.M., Geoffangen N.S.M., Geoffangen C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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Eukaryota: Fungi: Ascomycota: Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-FBB-2000 (Rel. 39, Last annotation update)
N-15'-PHOSPHORIBOSYL)ANTHRANILATE ISOMERASE (EC 5.3.1.24) (PRAI).
TRP1 OR YDRO07W.
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Murphy L., Richards C., Gentles S., Harris D., Barrell B.G.,
Rajandream M.A.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                             "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 124;
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Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E4D867EDA4FB4C3E CRC64;
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Pred. No. 1.21e+00;
14; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :: :|:::| |:: | |:| |:| | RVSGVLRLLALIFAIVTT-WMFIRSYMSF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; Transmembrane.
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14546 MW;
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Similarity 24.1%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                    Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
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Matches 7; Conser
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                                                                                                                                                                                                                                                                                                                                                                     [2]
IDENTIFICATION.
                                                                                                                                                                                                                                                                                                      influenzae Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                               Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRPF_YEAST
P00912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rigr;
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           RAPARA RAPARA PRAPARA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KAYKNSSGTPKYLVGVFRNQPKEDVLALVNDYGIDIVQLHGDESWQEYQEFLGLPVIKRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIMINIOGENETICS 44:446-452(1996).

-I-FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CANGES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

-I-SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-I-SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alvarez V., Coto E., Sehen F., Gouzalek-Koces S., Lopez-Larrea C., "Molecular evolution of the N-formyl peptide and C5a receptors in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
Snyder M., Buchman A.R., Davis R.W.;
Bent DNA at a yeast autonomously replicating sequence.";
"ature 324:87-89(1986).
-!- CATALYTIC ACTIVITY: N·(5'-PHOSPHORIBOSYL)-ANTHRANILATE
-!- CARBOXYPHENYLAMINO)-1-DESOXY-RIBULOSE 5-PHOSPHATE.
-!- PATHWAY: THIRD STEP IN TRYPTOPHAN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 95; DB 1; Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
N-FORMYL PEPTIDE RECEPTOR-LIKE 2 RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.21e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :| ::::| : | :: | | 173 GF-RDSWVFIGAKDLRGKSPFEQFLKNSPDTNKYEGW 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 VFPKDCNILLSAASQKPHSFIPLFDSEAGGTGELLDW 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                        EMBL; V01341; CAA24634.1; -. EMBL; J01374; AAA88758.1; -. EMBL; M74015; AAA72097.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z48008; CAA88068.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 5.6%;
Local Similarity 25.8%;
nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-human primates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 96421539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FML2_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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CONTROL
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062754;
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                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                        Query Match
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for commercial
     entities requires a license agreement (see http://www.isb-sib.ch/announce.or send an email to license@lsb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                           231 KRMTKSSRPLH-IFTAVVASFFICWF-PYELTGILMAVWL----KEILLNGKYKIILVLI 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bowen AR., Chen-Wu J.L., Momany M., Young R., Szaniszlo P.J.,
Robbins P.W.;
"Classification of fungal chitin synthases.";
Proc. Natl. Acad. Sci. U.S.A. 89:519-523(1992).
-: FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.
-: CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + [1,4-(N-ACETYL-
                                                                                                                                                                                                                                                                                                                                                             1 MRVSGVLRLIALIFAIVTTWMFIRSYMSFSMKTIRLPRWLASPTKEIQVK-KYKCGLIKP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang I., Graybill J.R., Szaniszlo P.J.;
"Characterization and expression studies of WdCHS3, a gene that encodes a class III chitin synthase and contributes to virulence in Wangiella (Exophiala) dermatitidis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exophiala dermatitidis (Wangiella dermatitidis).
Eukaryota, Fungi; Ascomycota; Chaetothyriales; Herpotrichiellaceae;
anamorphic Herpotrichiellaceae; Exophiala.
                                                                                                                                                                                                                                                                                                                                                                                                                                         CHS3_EXODE STANDARD; PRT; 885 AA.
B30602; O74678;
01-APR-1993 (Rel. 25, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CHITIN SYNTHASE 3 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL
TRANSFERASE 3) (CLASS-III CHITIN SYNTHASE 3).
                                                                                                                                                                                                                                                                                                                        6
and
                                                                                                                                                                                                                                                                                                    Length 349;
                                                                                                                                                                                                                                                                                                              No. 1.21e+00;
Mismatches 37; Indels
                                                                           G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
ρλ
                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                      6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                 C0C92A9E5CDE250C CRC64;
                                                                                                                                                                          5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                (POTENTIAL).
                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                              60 CPANYFAF-KICSGAANVVGPTMCFEDRMIMSPVKNNVGRGL 100
                                                                                                                                                                                                                                                                                                                                                                                  285 NPTSSLAFFNSCLNPSLYVFMGHNFQERLIRS-LPTSLERAL 325
 Usage
                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                         27; Mismatches
 modified and this statement is not removed.
                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                           2 (POTENTIAL)
                                                                                                         1 (POTENTIAL)
CYTOPLASMIC (
                                               GCR_1739; .
3; PS00237; G_PROTEIN_RECEPTOR; 1.
                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                      Score 95;
                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                   39531 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 214-410 FROM N.A.
                                                                                                                                                                                                                                                                                                      5.68;
                                                                                                                                                                                                                                                                                                               Local Similarity 28.4%;
les 29; Conservative
                                     EMBL; X97740; CAA66324.1;
                                                                                              27
50
61
83
83
100
100
140
162
205
                                                                                                                                                                                                                                     >349
                                                                   PFAM; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                   349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 92115692
                                                                                                      28
51
62
84
1101
1122
1141
1163
227
227
227
227
287
307
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                                                                                      Chemotaxis.
                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
                                                                                                                  DOMAIN
TRANSMEM
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TRANSMEM
DOMAIN
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TRANSMEM
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DISULFID
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TRANSMEM
                                                                                                       TRANSMEM
                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                       Query Match
                                                         PROSITE;
                                                                                                                                                                 FRANSMEM
                                                                                                                                                                                                        FRANSMEM
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                                                                                               DOMAIN
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mack by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY. SUBFAMILY CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Trichosurus vulpécula).";
Gen. Comp. Endocrinol. 111:68-75(1998).
-!- FUNCTION: GROWTH HORMONE PLAYS AN IMPORTANT ROLE IN GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLUIAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Metatheria; Diprotodontia; Phalangeridae; Trichosurus
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF053314; AAC35278.1; -.
BEMBL; MBH207; AAA30336.1; -.
EMBN; PF01644; Chitin. Synth; -.
Transferase; Glycosyltransferase; Transmembrane; Cell wall;
BETA-D-GLUCOSAMINYL)](N) = UDP + [1,4-(N-ACETYL-BETA-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                837 LVATWIFSNALLAVAITSDSLDRFGFTSEPLRGPAISSRRF-CGLLRPC 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brushtail possum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y -> M (IN REF. 2).
R -> S (IN REF. 2).
48D00BEE408398F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 983.25478.
Saunders M.C., Deakin J., Harrison G.A., Curlewis J.D.
"CDNA cloning of growth hormone from the brushtail pos
                         GLUCOSAMINYL)](N+1).
SUBCELLULAR LOCATION: PLASMA MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 95; DB 1;
Pred. No. 1.21e+0
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trichosurus vulpecula (Brush-tailed possum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOMATOTROPIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence updai
15-UUL-1999 (Rel. 38, Last annotation updai
SOMATOTROPIN PRECURSOR (GROWTH HORMONE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00266; SOMATOTROPIN_1: 1. PROSITE; PS00338; SOMATOTROPIN_2: 1. PFAM: PF00103; hormone; 1. Hormone; Pituitary; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 215 Y
340 340 R
885 AA; 99422 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00836; SOMATOTROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF052192; AAC08986.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.6%;
Local Similarity 28.6%;
les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
215
188
213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multigene family.
CONFLICT 215
CONFLICT 340
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77
205
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24353 MW; F241085B4A7352D1 CRC64;

215 AA;

SEQUENCE

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Escherichia.
  LT 13
DMSC_ECOLI
P18777;
                                                                    SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY.
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                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                         111 LSPVQF-LSRVFTNSLVFGTSDRVY-EKLRDLEEG-IQALMQELEDGSSRGGLVLKTTYD 167
                                               1 MAQRLLLRRFLTSIISGKPSQSRWAPVASRALKTPQYSPGYLTVTPSQARSIYTTRVCST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                       MEDLINE; 98028383.
Watabe S., Hiroi T., Yamamoto Y., Fujioka Y., Hasegawa H., Yago N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Gaps
                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
Bovinae; Bos
                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRION.
MITOCHONDRIAL THIOREDOXIN.
REDOX-ACTIVE (BY SIMILARITY).
5596F7DDA7E34D5F CRC64;
  Score 91; DB 1; Length 166;
Pred. No. 4.07e+00;
27; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                   'SP-22 is a thioredoxin-dependent peroxide reductase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00194; THIOREDOXIN; 1.
PFAM; PF00085; thiored; 1.
Redox-active center; Electron transport; Mitochondrion;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 60-106 AND 111-166.
TISSUE~ADRENAL CORTEX;
                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
MITOCHONDRIAL THIOREDOXIN PRECURSOR (MT-TRX).
                                                                                                                              166 AA.
 Score 92;
                                                                       168 KFDTNLRSDEALLKNYG-LLSCFKKDL 193
                                                                                166 AA; 18416 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D87741; BAA13447.1; -. PRINTS; PR00421; THIOREDOXIN.
Query Match 5.5%;
Best Local Similarity 32.2%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 5.4%;
Local Similarity 19.2%;
nes 15; Conservative
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                                                                                                                             STANDARD;
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166
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                                                                                                                                                                                                                                                                         Takahashi S.Y.
                                                                                                                  LT 12
THI2_BOVIN
Q95108;
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Weiner J.H., Shaw G., Turner R.J., Trieber C.A.;
Weiner J.H., Shaw G., Turner R.J., Trieber C.A.;
Weiner J.H., Shaw G., Turner R.J., Trieber C.A.;

Schology of the anchor subunit of dimethyl sulfoxide reductase of Escherichia coll.";

J. Blol. Chem. 268:3238-3344(1993).

-I-FUNCTION: TERMINAL REDUCTASE DURING ANAEROBIC GROWTH ON VARIOUS SULFOXIDE AND M-OXIDE COMPOUNDS. THE C SUBUNIT ANCHORS

THE OTHER TWO SUBUNITS TO THE MEMBRANE AND STABILIZE THE CATALYTIC
                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ANAEROBIC DIMETHYL SULFOXIDE REDUCTASE CHAIN C (DMSO REDUCTASE ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikamoto K., Ikada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 97426617.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the anaerobic
                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yano M., Horiuchi T.; "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: THE COMPLEX CONSIST OF THREE SUBUNITS: DMSA, THE REDUCTASE; DMSB, AN ELECTRON TRANSFER PROTEIN, AND DMSC, A MEMBRANE ANCHOR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-K12 / C660;
MEDLINE, 89096500.
Bilous P.T., Cole S.T., Anderson W.F., Weiner J.H.;
Wluclectide sequence of the disABC operon encoding the dimethylsulphoxide reductase of Escherichia coli.";
Mol. Microbiol. 2:785-795(1988).
287 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, J03412; AAAB3845.1; -.
EMBL, AAC73982.1; -.
EMBL, D90727; BAA35628.1; -.
EMBL, D90728; BAA35638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
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                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mau B., Shao Y.;
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335 SSIYVAAAHGCWGITLG 351

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 LPELSSDTKVDQDKCALIKQC-ANHFH-QIIRDSPVKVRQA-CYLPISNATGAPVIGKIG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Gaps
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=972;
Gentles S., Odell C., Churcher C.M., Barrell B.G., Rajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Walsh S.V.;
Submitted (NOV-1995) to the EWBL/GenBank/DDBJ databases.
-! - SUBCELJULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-! - SIMILARITY: TO YERST YHROUGC.
                                                                                                                                                                                                                                                                                                                   ij
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                                                                                                                                                                                                                                                                                       Score 91; DB 1; Length 287;
Pred. No. 4.07e+00;
                                                                                                                                                                                                                                                                                                                   13; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    YAM3_SCHPO STANDARD; PRT; 382 AA.
Q10058;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HYPOTHETICAL 41.5 KD PROTEIN CIF5.03C IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                 PERIPLASMIC (POTENTIAL).
DB6D26ACD2BE0CEB CRC64;
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COAF06F5534C3710 CRC64;
                                                                                                                  CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PERIPLASMIC (POTENTIAL).
POTENTIAL.
                                                                                       PERIPLASMIC (POTENTIAL). POTENTIAL).
                                        PERIPLASMIC (POTENTIAL).
                                                                                                                                                                     CYTOPLASMIC (POTENTIAL). POTENTIAL).
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                                                                 CYTOPLASMIC (POTENTIAL)
                             Inner membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane.
PIR; S03787; S03787.
ECOGENE; EG10234; DMSC.
Oxidoreductase; Transmembrane;
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Hypothetical protein; Transme
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Similarity 28.6%;
22; Conservative
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Best Local Similarity 23.5%;
Matches 8; Conservative
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382 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- PATHWAY: BRANCH-POINT REACTIONS BETWEEN GENERAL PHENYLPROPANOID METABOLISM AND PATHWAYS LEADING TO VARIOUS SPECIFIC END PRODUCTS.
-:- INDUCTION: TRANSCRIPTIONALLY ACTIVATED BY BOTH FUNGAL ELICITOR AND ULTRAVIOLET IRRADIATION.
-:- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                             Zhao Y., Kung S.D., Dube S.K.;
"Nucleotide sequence of frice 4-coumarate:CoA ligase gene, 4-CL.1.";
Nucleic Acids Res. 18:6144(1990).
"Incleic Acids Res. 18:6144(1990).
-i. CATALYTIC ACTIVITY: ATP + 4-COUMARATE + COA = AMP + PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, euphyllophytes, Spermatophyta, Magnoliophyta, Liliopsida, Poales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00501; AMP-binding; 1.
Ligase; Phenylpropanoid metabolism.
SEQUENCE 563 AA; 60841 MW; 35B329401C6B44B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
                                                                                                                                 01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
4-COUMARATE--COA LIGASE (EC 6.2.1.12).
                                                                                             563 AA
                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; JU0311; JU0311.
HSSP; P08659; 1LCI.
PROSITE; PS00455; AMP_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X52623; CAA36850.1; -. PIR; JU0311; JU0311.
98 RGLNIALVNGTTGAVLG 114
                                                                                             STANDARD;
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STRAIN=CV. JAPONICA;
MEDLINE; 91045096.
                                                                                                                                                                                                                                      Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                 Poaceae; Oryza
                                                                          LT 15
4CL_ORYSA
P17814;
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Search completed: Wed May 31 11:04:38 2000 Job time: 12 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 14.02 Seconds 750.250 Million cell updates/sec Wed May 31 11:03:51 2000; Run on:

Tabular output not generated.

>US-09-186-342-2 (1-223) from USO9186342.pep 1686 1 MRVSGVLRLLALIFAIVTTW......KYEGWPELLEMEGCMPPKPF 223 Title: Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

142080 segs, 47172406 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir62 1:pir1 2:pir2 3:pir3 4:pir4 Database:

scale 0.498 Variance 93.300; Mean 46.426; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	2.76e-154	6.73e-02	1.23e-01	9.50e-01	7.13e-01	7.13e-01	1.68e+00	2.93e+00	2.93e+00	3.87e+00	3.87e+00	3.87e+00	3.87e+00	5.09e+00	6.67e+00	1.14e+01	8.74e+00	1.14e+01	8.74e+00	1.49e+01	1.49e+01	1.49e + 01	1.49e+01
	Description	gene 2.19 protein - h	CREB-binding protein	potassium channel pro	hypothetical protein	kakapo gene protein i	kakapo gene protein -	hypothetical protein	probable n2, n2-dimeth	molybdopterin-binding	hypothetical protein	hypothetical protein	glycylpeptide N-tetra	immunodominant type-s	phosphoribosylanthran	hypothetical protein	hypothetical protein	hypothetical protein	hypothetical protein	two-component sensor	hypothetical protein	probable dimethylsulf	hypothetical protein	4-coumarateCoA liga
	A	137095	T13828	T13807	C69288	T13715	T13714	869859	C75153	G69269	T15631	T15849	T00697	B42804	ISBYN	T10665	T03886	C70357	S51348	B70047	F72500	S03787	C75078	JU0311
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	Match Length DB	230	3190	1001	253	2285	2396	121	383	1134	269	320	389	522	224	852	291	469	509	573	257	287	491	263
% Ouerv	Match	53.9	6.5	6.4	0.9	0.9	0.9	5.9	5.8	5.8	5.7	5.7	5.7	5.7	5.6	5.6	5.5	5.5	5.5	5.5	5.4	5.4	5.4	5.4
	Score	806	110	108	101	102	102	66	26	97	96	96	96	96	95	94	92	93	92	93	91	91	91	91
Result	NO.		7	٣	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

microbial collagenase 1.49e+01 SIL protein - human 1.49e+01 ArtA Protein - Escher 2.51e+01 hypothetical protein 1.94e+01 somatotropin precurso 2.51e+01 28.5K transport protein 1.94e+01 28.5K transport protein 1.94e+01 copD homolog - xantho 2.51e+01 NADH dehypdrogenase su 2.51e+01 probable oxidoreducta 1.94e+01 probable oxidoreducta 1.94e+01 probable oxidoreducta 1.94e+01 probable correspondings 1.94e+01 sapartate transaminas 1.94e+01 chhosphofructo-2.kin 1.94e+01 chhosphofructo-2.kin 1.94e+01 chpoptide transport pro 2.51e+01 peptide transport pro 2.51e+01 peptide transport pro 2.51e+01 peptide transport pro 2.51e+01 peptide cleavage and 1.94e+01 glibon ape leukemia r 2.51e+01 leukemia virus recept 2.51e+01	gene 2.19 protein - human #forman_name man #forman_name Homo sapiens #common_name man #forman_name Homo sapiens #common_name man #forman_name Homo sapiens #common_name man 0.1 Nov-1996 #fecquence_revision 01-Nov-1996 #text_change 28-Feb-1997	complete ein homolog – fruit fly (Drosophila
2 JC4393 2 A41685 1 B4VEGAA 1 B4VEGAA 2 S07957 2 S07957 1 INTMU2 2 D36868 2 A40734 2 F70933 2 A40734 2 F70933 2 A40809 2 T11166 2 T04378 2 C72749 2 C72749 2 I52822 3 A40804 2 I52822 3 A40804 3 A40804 4 I168084	137095 #type complete gene 2.19 protein - human #formal_name Homo sapiens # 01-Nov-1996 #sequence_revis. 28-Feb-1997 137095 137095 Bione, S.; Tamanini, F.; Mar Poustka, A.; Torri, G.; R. Proc. NaLL. Acad. Sci. U.S.: Transcriptional organization X chromosome in Xq28. 137095 137095 Dreliminary; translate preliminary; translate se MUD:94068527 137095 preliminary; translate 12.19 #length 230 #molecular-well #length 230 #lill #li Conservative 56; Mismat GPLRIVALVASVGAANVIGPRICLEDKMLM WMAGDVNDLLKFIRPLHEGTLVFVASYDDP	T13828 #type comp CREB-binding protein
1282 1287 1287 1304 1304 1304 1305 1307 1307 1307 1307 1307 1307 1307 1307	137095 #type gene 2.19 proteil #formal_name Hom 0.Now-1996 #seq 1.87095 137095 137095 137095 137095 Proc. Mail. Acad Transcriptional & Achonosome il X chromosome il X chromosome il X chromosome il Y chromosome il 137095 preliminary preliminary preliminary preliminary preliminary preliminary preliminary 1-230 ##lab ferences EMBL:X87 2.19 #length 230 #mo 53.3%; Conservative LRIVALVEVGVENIVY :: :: :: : EBHLAERVVSGGANVIG SGDVMLLKEIRFLHEG AGDVNDLLKFIRFLHEG :: :: : GANDLLKFIRFLHEG AGDVNDLLKFIRFLHEG :: : : GANDLLKFIRFLEG	3828 EB-bindin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GGMQQVVGTQMGMVNSMPMS-ISNNGNNGMNAIPGMNTIAQGNLGNMVLTNSVGGGMGGM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 FFAFTVCSTVGYGNISPTT-FAGRMIMIAY-SVIGIPVNGILFAGL-GEYFG-RTFEAIY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; Goodman, R.H.; Ishii, S. Nature (1997) 386:735-738
Drosophila CBP is a co-activator of cubitus interruptus
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
           #formal_name Drosophila melanogaster
20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
20-Sep-1999
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13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change
13-Aug-1999
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SUMMARY #length 3190 #molecular-weight 331879 #checksum 2759
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SUMMARY #length 1001 #molecular-weight 109289 #checksum 4583
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hypothetical protein AF0307 - Archaeoglobus fulgidus
#formal_name Archaeoglobus fulgidus
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Pred. No. 1.23e-01;
14; Mismatches 20; Indels 6;
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potassium channel protein - fruit fly (Drosophila
                                                                                                                                                                                                                                                               ##residues 1-3190 ##label AKI
##cross-references EMBL:U88570; NID:91916929; PID:91916930;
PIDN:AAB53050.1
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#cross-references MUID:97075152
#accession T13807
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melanogaster)
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Best Local Similarity 33.3%;
Matches 20; Conservative
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Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; F. Ketchum, R.J.; Rainayage, A.R.; Graham, D.E.; Kyrpides, N.C.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocsyne, J.D.; Weidman, J.F.; McDonald, L.; Utterback, R.; Gocsyne, J.D.; Weidman, J.F.; Artlach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujil, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross-references GB:AE001083; GB:AE000782; NID:g2689406; PID:g2650329; TIGR:AF0307

* length 253  #molecular-weight 30215  #checksum 6275
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J. Cell Biol. (1998) 143:1271-1282
Kakapo, a gene required for adhesion between and within cell
layers in Drosophila, encodes a large cytoskeletal linker
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melanogaster) (fragment)
#formal_name_Drosophila melanogaster
13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #fitle The complete genome sequence of the hyperthermophilic,
sulfate-reducing archaeon Archaeoglobus fulgidus.
#cross-references MUID:98049343
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Pred. No. 9.50e-01;
15; Mismatches 21; Indels
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Best Local Similarity 33.9%;
Matches 21; Conservative
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J. Cell Biol. (1998) 143:1271-1282
Kakapo, a gene required for adhesion between and within cell
layers in Drosophila, encodes a large cytoskeletal linker
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                                                                                                                                 kakapo gene protein - fruit fly (Drosophila melanogaster)
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23-Aug-1996 #sequence_revision 06-Sep-1996 #text_change
21-Nov-1997
869859
                                                                                                                                                             #formal_name Drosophila melanogaster
13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change
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hypothetical protein YMR075c-a - yeast (Saccharomyces
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SUMMARY #length 121 #molecular-weight 14033 #checksum 4865
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1-73396 ##1EASIGUES
##cross-references EMBL:AJ011924; NID:e1332040; PID:e1332041;
PIDN:CAA09869.1
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Pred. No. 1.68e+00;
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Pred. No. 7.13e-01;
22; Mismatches 25; Indels
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llarity 35.5%;
Conservative
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Matches 11; Conser
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                             QFLAMGPE 916
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QFLKNSPD 201
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Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; Deterson, J.D.; Richardson, D.L.; Kerlavage, A.R.; Graham, D.E.; Kyrpides, N.C.; FleisChmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; MoNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.

Nature (1997) 390:364-370

The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon Archaeoglobus fulgidus.
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molybdopterin-binding oxidoreductase homolog - Archaeoglobus
                                                                                                                                                                                                                                                                                                  anonymous, Genoscope
by the EMBL Data Library, July 1999
Pyrooccus abysi genome sequence: insights into archaeal
chromosome structure and evolution.
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C75153 #type complete probable n2,n2-dimethylguanosine tRNA methyltransferas PAB2092 - Pyrococcus abyssi (strain Orsay) #formal_name Pyrococcus abyssi 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
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05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
05-Jun-1998
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#length 383 #molecular-weight 43218 #checksum 9956
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Pred. No. 2.93e+00;
28; Mismatches 26; Indels
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Pred. No. 2.93e+00;
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Local Similarity 21.6%;
Les 16; Conservative
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Best Local Similarity 27.3%;
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                               990 VVAAVEPTVVKGTIAIPVGMGRWADSAVKKPAYFRLNDGSVAALVS---ELPDGA-SLPS 1045
                                                88 IMSPVKNNVGRG-LNIALVNGT-TGAVLGQKA-FDMYSGDVMHLVKFLKEIPGGALVLVA 144
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    Gaps
                                                                                                                                                                              hypothetical protein C56C10.9 - Caenorhabditis elegans #formal_name Caenorhabditis elegans 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 15849
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31/3; 68/3; 140/3; 188/3
#length 269 #molecular-weight 31750 #checksum 2802
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#length 320 #molecular-weight 37556 #checksum
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                                                                                                                                                                                                                                                                                                                                                   preliminary; translated from GB/EMBL/DDBJ
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PIDN:AAA68788.1; CESP:C25H3.10
##experimental_source strain Bristol N2
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 Mismatches 40; Indels
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Pred. No. 3.87e+00;
32; Mismatches 43; Indels
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                                                                                         1046 DAVNPVKQLDETKKRILFTKSDRRYYDDLGI-DSWRFSG 1083
                                                                                                         Score 96; DB 2; I Pred. No. 3.87e+00;
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   23;
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Local Similarity 37.8%;
les 17; Conservative
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Best Local Similarity 20.4%;
Matches 21; Conservative
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##residues 1-32
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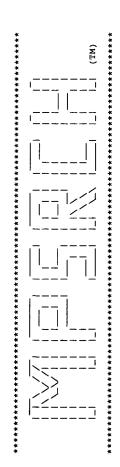
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Ohashi, N.; Nashimoto, H.; Ikeda, H.; Tamura, A.
J. Biol. Chem. (1992) 267:12728-12735
Diversity of immunodominant 56-kDa type-specific antigen
(TSA) of Rickettsia tsutsugamushi. Sequence and comparative
analyses of the genes encoding TSA homologues from four
antigenic variants.
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                                                                                                                                        Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kerlavag A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C. submitted to the EMBL Data Library, June 1998 Arabidopsis thaliana chromosome II BAC F6E13 genomic
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                                                                                                                                                                                                                       #formal_name Arabidopsis thaliana #common_name mouse-ear
                                                                                                                                                                                                                                                                     01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change
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04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
20-Mar-1998
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#length 522 #molecular-weight 55971 #checksum 2488
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##experimental_source cultivar Columbia
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#length 389 #molecular-weight 44450 #checksum
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Pred. No. 3.87e+00;
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##cross-references GB:M63383; NID:q152512; PID:q152513
##experimental_source strain Kawasaki
                            : :: :: | : | : | : | : | : | : | 176 DSWVFIGAKDLR--GKSPFE-QFLKNSPDTNKYEGWPELLEME 215
260 ELYDYVDPQNFRLASKEVNDIMMLTDANNDEKL-SLEELLERD 301
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Pred. No. 3.87e+00;
7; Mismatches 8;
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Best Local Similarity 31.0%;
Matches 18; Conservative
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Best Local Similarity 48.5%;
Matches 16; Conservative
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T00697
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##residues 1-3
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#accession B428
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#accession
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##residues 68-224 ##label MUW
##cross-references EMBL:Z48008; NID:G642799; PIDN:CAA88068.1;
PID:e159531; PID:g1326006
##note due to an ochre mutation the TRP1 gene is split into two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
##residues_type DNA
##residues_1-57, 59,66 ##label MUR
##cross-references EMBL:Z48008; NID:g642799; PIDN:CAA88067.1;
##note due to an ochre mutation the TRP1 gene is split into two
parts in this strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                phosphoribosylanthranilate isomerase (EC 5.3.1.24) - yeast GSaccharomyces constraine)
protein YDB119.13A; protein YDB119.13B; protein YDB007w
#formal_name Saccharomyces cerevisiae
118-mar-1999
118-min-1999
118-min-1999
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                                                                                                                                                                                                                                                                                           Tschumper, G.; Carbon, J. Gene (1980) 10:157-166 Sequence of a yeast DNS fragment containing a chromosomal replicator and the TRP1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T10665 #type complete
hypothetical protein F6E21.30 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
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#map_position 4R
CLASSIFICATION #superfamily phosphoribosylanthranilate isomerase; trpF
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16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
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                      252 VLSDKITQIYS-DIRQFAKIANIEVPGAPLPNSASVEQIQTKMQELN-DVLEELRESF 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.6%; Score 95; DB 1; Length 224; Best Local Similarity 25.8%; Pred. No. 5.09e+00; Matches 25; Conservative 21; Mismatches 47; Indels
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#length 224 #molecular-weight 24158
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#accession A01135
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#title
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                                                       Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemkek, K.; Schueller, C. submitted to the Protein Sequence Database, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       762 GLLDLIGQELCFRERIHMGNVHSGK-RAMVISSLKKANISASRKQRIKLEINGEKELTFS 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                              2864
                                                                                                                                                                                                                ##cross_references EMBL.AL049914; GSPDB:GN00062; ATSP:F6E21.30
##experimental_source cultivar Columbia; BAC clone F6E21
                                                                                                                                                                                                                                                                                                                                                                                                                                .;
                                                                                                                                                                                                                                                                                                                                                   #checksum
                                                                                                                                                                                                                                                                                                                                                                                     Score 94; DB 2; Length 855;
Pred. No. 6.67e+00;
23; Mismatches 31; Indels
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#length 855 #molecular-weight 95591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: Wed May 31 11:04:09 2000 Job time: 18 secs.
                                                                                                                                                                                                   1-855 ##label BEV
                                                                                                                                                    ##molecule_type DNA
##residue
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Best Local Similarity 24.0%;
Matches 18; Conservative
20-Sep-1999
T10665
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#introns
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed May 31 11:05:38 2000; MasPar time 6.14 Seconds 524.106 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-186-342-2 (1-223) from USO9186342.pep 1686 1 MRVSGVLRLLALIFAIVTTW......KYEGWPELLEMEGCMPPKPF 223 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

145341 seqs, 14437480 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Mean 30.975; Variance 139.082; scale 0.223

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	1.52e-80	1.52e-80	1.59e+00	4.40e+00	2.70e+01	3.72e+01	3.72e+01	3.72e+01	6.01e+01	7.03e+01	7.03e+01	7.03e+01	8.23e+01	8.23e+01	8.23e+01	8.23e+01	7.03e+01	9.63e+01	9.63e + 01	9.63e + 01	9.63e + 01	9.63e + 01	9.63e+01
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;	ID	PCT-US95-0	US-08-469-	US-08-332-	US-08-468-	US-08-775-	ns-08-868-	US-07-674-	US-08-436-	US-08-731-	US-08-478-	US-07-881-	US-08-120-	PCT-US95-0	US-08-249-	-988-80-Sn	ns-08-100-	US-08-737-	us-07-885-	us-08-093-	US-08-459-	US-08-383-	US-07-801-	US-09-105-
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1	Length	135	135	618	993	166	614	680	680	731	92	97	92	119	119	119	433	671			193	193	199	217
Query	Match	58.9	58.9	6.4	9.0	5.4	5.3	5.3	5.3	5.1	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	4.9	4.9	4.9	4.9	4.9	4.9
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		82 4.9 444 82 4.9 531 82 4.9 531 82 4.9 627 82 4.9 627 83 4.9 627 83 4.9 629 83 4.9 629 83 4.9 2104 83 4.9 2104 83 4.9 2104 81 4.9 2104 81 4.9 2104 81 4.9 2104 81 4.9 2104 81 4.8 687 81 4.8 687 81 4.8 687 81 4.8 687 81 4.8 687 81 4.8 687	ALIGNMENTS	SULT 1 PCT-US95-07289-7 STANDARD;	Sequence 7,	Sequence 7, Application PC/TUS9507 GENERAL INFORMATION: APPLICANT: YV, Guo-Liang APPLICANT: Nose, Claid TITLE OF INVENTION: Colon Spec NUMBER OF SEQUENCES: 24 COMRESPONDENCE ADDRESS: ADDRESSEE: Stewart & Olstein STREET: 6 Becker Farm Road CITY: Roseland STATE: NJ COUNTRY: USA ZIP: 07068-1739 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS- SOFTWARE: PATENTIN Release # CURRENT APPLICATION DATE: 06-UNN-1995 GILLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: Ferrarc, Gregory D. REGISTRATION NUMBER: 335,134 RECISTRATION NUMBER: 335,134 RECISTRATION NUMBER: 335,134 RECISTRATION NUMBER: 335,134 RECISTRATION NUMBER: 335,134 RECOMMUNICATION NUMBER: 335 TELEPHONE: 201-994-1704 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 135 amino acids TYPE: amino acid TYPE: amino acid TYPE: Applicatype: protein SEQUENCE 135 AA; 14852 MW; 99029

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US-08-332-312-2
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APPLICANT: Rosen, Craig
TITLE OF INVENTION: Colon Specific Genes and Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
  Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 135;
Score 993; DB 4; Length 135
Pred. No. 1.52e-80;
0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA
                                                                                                                                                     135 AA.
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Pred. No. 1.52e-80;
0; Mismatches 0;
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NAME: FETTERCY, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-435
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-994-1704
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/469,667
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
JENCE 135 AA; 14852 MW; 99029 CN;
                                                                                                                                                                                                                    Sequence 7, Application US/08469667 Patent No. 5733748 GENERAL INFORMATION:
                                                                                                                                                                                                     Sequence 7, Application US/08469667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ 1D NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 135 amino acids TYPE: amino acid
                                                                                                                                                     STANDARD;
Query Match 58.9%;
Best Local Similarity 100.0%;
Matches 135; Conservative
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Best Local Similarity 100.0%;
Matches 135; Conservative
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CITY: Roseland
STATE: NJ
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Sequence 2, Application US/08332312
Patent No. 5559026
GENERAL INFORMATION:
APPLICANT: Price, Laura A.
APPLICANT: Pausch, Mark H.
TITLE OF INVENTION: Functional Expression of a Drosphila
TITLE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                      61 PGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKDLRGKSPFEQFLKNSPDTNKYEGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 FFAFTVCSTVGYGNISPTT-FAGRMIMIAY-SVIGIPVNGILFAGL-GEYFG-RTFEAIY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,312
                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 108; DB 1; Dred. No. 1.59e+00; 14; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    993 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 618 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECCLE TYPE: protein
JENCE 618 AA; 70255 MW; 1951401 CN;
                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: P-38,711
REFERENCE/DOCKET NUMBER: 32,421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08332312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 6.4%;
Local Similarity 33.3%;
Les 20; Conservative
                                                                                  121 PELLEMEGCMPPKPF 135
                                                                                                         209 PELLEMEGCMPPKPF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Jersey
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1 MAQRILLERRFLTSIISGKPSQSRWAPVASRALKTPQYSPGYLTVTPSQARSIYTTRVCST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.4%; Score 91; DB 2; Length 166; Best Local Similarity 19.2%; Pred. No. 2.70e+01; Matches 15; Conservative 27; Mismatches 31; Indels
                                                                                                                   SOFTWARE: PastSEQ for Windows Version 2.0 SOFTWARE: PastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,978
FILING DATE: TO Be Assigned PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATION DATE:
ATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          614 AA.
                          ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0176 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             166 AA; 18416 MW; 148927 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VASANTHA NAGARAJAN
MARK S. PAYNE
STEPHEN K. PICATAGGIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/08968563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARLES E. NAKAMURA
ANTHONY A. GATENBY
AMY (KUANG-HUA) HSU
RICHARD D. LA REAU
SHARON L. HAYNIE
MARIA DIAZ-TORRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08968563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DONALD E. TRIMBUR GREGORY M. WHITED
                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO: 3:
                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                         LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
  NUMBER OF SEQUENCES: 3
                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |: |: |:| | 73 AANVGPTMCFEDRMIMS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TFNIQDGPD-FQDRVVNS 77
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                      GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6013494
GENERAL INFORMATION:
APPLICANT: CHARLES
                                               Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: GenBa
CLONE: 1545817
                                                                       USA
                                                            STATE: CA
COUNTRY: US,
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-968-563-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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                     Sequence 2, Application US/08468557
Patent No. 5759833
GENERAL INFORMATION:
APPLICANT: Shiba, Kiyotaka
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: Human Isoleucyl-tRNA Synthetase
TITLE OF INVENTION: Proteins, Nucleic Acids and Tester Strains Comprising Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               887 VIEPGLLFEIIEMLQSEETSSTSQ-LN-ELMMASESTLLAQEPREM-TADVIELKGKFLI 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 102; DB 1; Length 993
Pred. No. 4.40e+00;
23; Mismatches 23; Indels
                                                                                                                                         ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: U$/08/468,557 FILING DATE: 06-JUN-1995 CLASSIFICATION: 435 APPLICATION DATA: APPLICATION NUMBER: U$ 08/250,852 FILING DATE: 27-MAY-1994 ATCRNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08775978
Patent No. 5831049
GENERAL INFORMATION:
APPLICANT: GOLI, SURYA K.
APPLICANT: GOLI, SURYA K.
TITLE OF INVENTION: NOVEL HUMAN THIOREDOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 AA
                                                                                                                                                                                                                                                                                                                                                                                                    CPI94-13A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
ENCE 993 AA; 111800 MW; 5344624 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08775978
Sequence 2, Application US/08468557
                                                                                                                                                                                                                                                                                                                                                                           NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP1
                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 6.0%;
Local Similarity 30.1%;
es 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: || : :||
134 EIPGGALVLVASY 146
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                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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81 VSETIRKGLIDVEMYNSTQGLLMAGSVSAMFGSAVWQLVASFLK-LPISGTHCIVGA 136
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Patent No. 5874264
GENERAL INFORMATION:
APPLICANT: O'Hara, Bryan M.
TITLE OF INVENTION: Glabon Ape Leukemia Virus Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
CONTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.3%; Score 89; DB 1; Length 680; Best Local Similarity 28.1%; Pred. No. 3.72e+01; Matches 16; Conservative 20; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ź
                                                                                                                                                                                  OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII converted from IBM DW4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/674,287B
FILING DATE: 19910325
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
   ADDRESSEE: Dr. Karen A. Lowney
ADDRESSEE: American Cyanamid Company
STREET: 1937 West Main Street
STREET: P.O. BOX 60
                                                                                                                                                                                                                                                                                                                                                                                        31,104-01
                                                                                                                                                                                                                                                                                                                                                 NAME: LOWNEY, KAITEN A., Dr.
REGISTRATION NUMBER: 31,274
REFRENCE/DOCKET NUMBER: 31,104-01
TELEPHONE: 203 321 2361
TELEPHONE: 203 321 2971
TELEFAX: 203 321 2971
TELEFAX: 204 321 2971
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 680 Amino Acid Residues
TYPE: AMINO ACID SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: Protein
JENCE 680 AA; 73675 MW; 2557540 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08436900A
                                                                                  STATE: CT
COUNTRY: USA
ZIP: 06904-0060
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC AT
                                                                                                                                                                                                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                      Stamford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-436-900A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 89; DB 3; Length 614;
Pred. No. 3.72e+01;
11; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 DAATRGLNVALVEKGDFASGTSSKSTKMIHGGVRYLEKAFWEFSKAQLDLV
                                                                                                                                                                                                                                                                COUNTER TEADABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: 15.0 INCH DISKETTE
COMPUTER: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,563
APPLICANT: RAMESCH V. NAIR
TITLE OF INVENTION: METHOD FOR THE RECOMBINANT
TITLE OF INVENTION: PRODUCTION OF 1,3-PROPANEDIOL
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: MILMINGTON
STREET: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       680 AA
                                                                                                                                   STATE: DELAWARE
COUNTRY: U.S.A.
21P: 19898
ADDRESSEE: GENENCOR INTERNATIONAL, INC.
STREET: 4 CAMBRIDGE PLACE
STREET: 1870 SOUTH WINTON ROAD
CITY: ROCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/07674287B
Patent No. 5414076
GENERAL INFORMATION:
APPLICANT: Bryan Mark O'Hara
TITLE OF INVENTION: Gibbon Ape Leukemia
TITLE OF INVENTION: Virus Receptor
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,601
FILING DATE: NOVEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      614 AA; 68811 MW; 2001065 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/07674287B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEPAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 614 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.3%;
Best Local Similarity 35.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                        NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GUT 2
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                                                                                                                                                                                                                                       CITY: 1
STATE:
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Gaps

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SEQUENCE CHARACTERISTICS:
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                                               SEQUENCE
                                                                                                                                                                                                                                 XXXXXX
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                                                                                                                                                                                                                                                  | :: :|| :: :|: :|: :|: | ::: | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | 92 VRNNVGRGL-NIALVNGTTGAVLGQKAFDMYSGDVMHLV-KFLKEIP-GGALVLVAS 145
                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08731716
Patent No. 5789202
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jaskunas, S. Richard
APPLICANT: Rockey, Pamela K.
APPLICANT: Rosteck, Paul R. Jr.
APPLICANT: Rosteck, Paul R. Jr.
APPLICANT: No. 5789202115, Franklin H.
TITLE OF INVENTION: Streptococcus Pneumoniae
                                                                                                                                                                                                / Match 5.3%; Score 89; DB 2; Length 680; Local Similarity 28.1%; Pred. No. 3.72e+01; es 16; Conservative 20; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, VEISION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/731,716
                                                                                                                                                                                                                                                                                                     731 AA
                                    ATTORNEY AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,104-03
TELEPHONE: 201-683-2158
TELEPHONE: 201-683-2158
TELEPHONE: 201-683-2158
TELEPHONE: 201-683-2158
TELEPHONE: 201-683-2158
LENGTH: 680 amino acids
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,900A
FILING DATE: 08-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: x-10,887
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                    MOLECULE TYPE: protein
SEQUENCE 680 AA; 73675 MW; 2557540 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Eli Lilly and Company
STREFT: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                     PRT:
                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08731716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.
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                                                                                                                                                                                                                                                                                                   US-08-731-716-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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Sequence 9, Application US/08478675
Patent No. 577346
GENERAL INFORMATION:
APPLICANT: KEENE, JACK D.
APPLICANT: LEVING, PETER H.
APPLICANT: LEVING, PETER H.
APPLICANT: LEVING, PETER H.
APPLICANT: LEVING, PETER H.
APPLICANT: INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACID TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION NUMBER OF SEQUENCES: 101
                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                            472 ATVNDEGVDKAFEAGEKFGLNMEKVDRVLGVALGSGVETNPLQMAQAYAAFANEGLMPEA 531
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: VICTOR SPINAR, MCCLELLAND, MAIER & NEUSTAL STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia COUWTRY: U.S.A.

ZIP: 22202
COMPUTER: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,675
FILING DATE: US/08/478,675
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/120,827
FILING DATE: 15-SEP-1993
ATTONREY/AGENT INFORMATION:
NAME: Oblon, NO. 577346man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                   Score 86; DB 1; Length 731;
Pred. No. 6.01e+01;
24; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24,618
BER: 714-158-0 CIP
                                                                MOLECULE TYPE: protein
JENCE 731 AA; 80798 MW; 2731494 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                               532 HFISRIENASGQVIASHKNSQKRVIDKS 559
                                                                                                                                                                                                                                                                                                                                                             |: | :: :: | | :: | | | 130 KFLKEIPGGALVLVASYDDPGTKMNDES 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08478675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : (703)413-3000
(703)413-2220
  731 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 76 amino acids
TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                        Query Match 5.1%;
Best Local Similarity 21.6%;
Matches 19; Conservative
                        amino acid
                                               linear
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US-08-478-675-9
                                          TOPOLOGY:
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LENGIH:
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TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE TITLE OF INVENTION: RECGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACID TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION COMBES OF SEQUENCES: 10.1
CORRESPONDENCE ADDRESS:
       102 IALVNGTTGAVL-GQKAFDMYS--GDVMHLVKFLKEIPGGALV-LVASYD-DPG-TKMND 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VLMVYGLDQSKMNGDRVFNVFCLYGNVEK-VKFMKSKPGAAMVEMADGYAVDRAITHLNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: VIEGIAIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 85; DB 1; Length 76;
Pred. No. 7.03e+01;
19; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5525495man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 714-158-0 CIP
TELECOMUNICATION:
TELECHONE: (703)413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/120,827
ELLING DATE: 15-SEP-1993
CLASSIFICATION: 435
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                              Sequence 9, Application US/08120827
Patent No. 5525495
GENERAL INFORMATION:
APPLICANT: KEENE, JACK D.
APPLICANT: KING, PETER H.
APPLICANT: LEVINE, TODD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
JENCE 76 AA; 8481 MW; 29179 CN;
                                                                                                                                                                                                                                                Sequence 9, Application US/08120827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703)413 cc.
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.0%;
Best Local Similarity 29.5%;
Matches 18; Conservative
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US-08-120-827-9
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Patent No. 5444149

CENERAL INFORMATION:
CENERAL OF INVENTION:
CENERAL OF INVEN
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                                                                                                                        1 VLMVYGLDQSKMNGDRVFNVFCLYGNVEK-VKFMKSKPGAAMVEMADGYAVDRAITHLNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                       7;
                                  Score 85; DB 1; Length 76; Pred. No. 7.03e+01; 19; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 85; DB 1; Length 76;
Pred. No. 7.03e+01;
19; Mismatches 17; Indels
                                                                                                                                                                                                                                                                             76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NÜMBER: 714-154-0
TELECAMUNICATION INDORMATION:
TELEPHONE: (703)513-4500
TELEFAX: (703)486-2347
TELEX: 24855 Opar UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             PRT;
76 AA; 8481 MW; 29179 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LE TYPE: peptide
76 AA; 8481 MW; 29179 CN;
                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/07881075
                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 amino acids
                              Query Match 5.0%;
Best Local Similarity 29.5%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.0%;
Best Local Similarity 29.5%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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SEQUENCE
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RESULT

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47 EIVRGATGLMTGAGDPSAVVN-VIRKLDPEVGKNY--ELGWKDGAETKGVDATLNVNNIF 103
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Patent No. 5824321
GENERAL INFORMATION:
APPLICANT Heake, David A.
TITLE OF INVENTION: CLONED leptospira OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
PATENT NO. 5643754
GENERAL INFORMATION:
APPLICANT: HEAKE, David A.
TITLE OF INFURITION: CLONED LEPTOSPITA OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 84; DB 1; Length 119; Pred. No. 8.23e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Mismatches 27; Indels
                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,013
FILING DATE: 25-MAY-1994
                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 AA
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PD-3602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 AA; 12942 MW; 73190 CN;
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Tumarkin Ph.D., Lisa A.,
REGISTRATION NUMBER: P-38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08886863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein IMMEDIATE SOURCE:
                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.0%;
Best Local Similarity 29.3%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : :|: | :|:
193 EQ-FLKNSPDTNKYE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 DKKYPRNATVTLRYD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                  90067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-886-863-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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           47 EIVRGATGLMTGAGDPSAVVN-VIRKLDPEVGKNY--ELGWKDGAETKGVDATLNVNNIF 103
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                                                                                                                                Sequence 8, Application PC/TUS9506764
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: CLONED leptospira OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 84; DB 4; Length 119;
Pred. No. 8.23e+01;
21; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: PCT/US95/06764
FILING DATE: 25-MAY-1995
                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson STREET: 4225 Executive Square, Suite 1400 CITY: La JOlla STATE: California COUNTRY: USA
           119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:

NAME: Haile, Ph.D., Lisa A.,
REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: FD3602

TELEPHONE: (619) 678-5070

TELEPAX: (619) 678-5070

TELEPAX: (619) 678-5070

TELEPAX: (619) 678-509

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 AA; 12942 MW; 73190 CN;
                                                                                                       Sequence 8, Application PC/TUS9506764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08249013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 119 amino acids
           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.0%;
Best Local Similarity 29.3%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : : |: | : |:
193 EQ-FLKNSPDTNKYE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 DKKYPRNATVTLRYD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                 92037
           PCT-US95-06764-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-249-013-8
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ZIP: 90067

ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/249,013
FILING DATE: 01-JUL.1997
CLASSIFICATION NUMBER: US 08/249,013
FILING DATE: D-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: TUMBER: P-38,347
REFERENCE/DOCKET NUMBER: P-38,347
REFERENCE/COCKET NUMBER: P-38,347
REFERENCE/COMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 annino acids
STRANDEDENESS: single
TOPOLOGY: 11near
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: PUPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.0%; Score 84; DB 2; Length 119; Best Local Similarity 29.3%; Pred. No. 8.23e+01; Matches 22; Conservative 21; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
LOCATION: 1
VCE 119 AA; 12942 MW; 73190 CN;
   Los Angeles
California
                                 USA
CITY: LOS
STATE: CZ
COUNTRY:
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104 DKKYPRNATVTLRYD 118 : : | : |: | : |: | 193 EQ-FLKNSPDTNKYE 206 a ŝ

47 EIVRGATGLMTGAGDPSAVVN-VIRKLDPEVGKNY--ELGWKDGAETKGVDATLNVNNIF 103

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5; Gaps

Search completed: Wed May 31 11:05:48 2000 Job time : 10 secs.

Sequence:

Run on:

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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                       4857316 seqs, 2026611650 residues
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                                                                                     OM nucleic - nucleic search, using sw model
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Listing first
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Maximum DB seq length: 1000000
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Perfect score:
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9D_est28:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

	FEATURES	BASE COUNT ORIGIN	Query Matcl Best Local Matches 18	Oy 355 ga; Db 645 GA; Oy 415 gc; Db 585 gc]		OY 595 WSI DD 405 AGG OY 655 CCT OY 655 CCT DD 345 CCC LOCUS AW001287/C LOCUS DEFINITION ACCESSION VERYWORDS SOURCE ORGANISM E REFERENCE ATHORS ATHORS
Description AW300770 xk05902.x AW301287 wu27e06.x AA297147 EST112731 A1883327 fc60e01.y AW323823 u077a04.y A1691072 wf22c03.x A1691072 wf22c03.x A1691072 wf22c03.x AA611725 v089f11.r AA297176 EST112740	AA298484 EST114112 AA451058 V186607.r AA55393 nk23b02.s NA1338 yw68g05 r1 AW175415 ff135h03.y H26710 y144b12.r1 AA622758 np76c04.s AW455134 E8611267 AA793766 vr96e04.r A1245950 qk45b04.x AW369250 Qv1-BN000 A1348065 qp56d09.x AA592348 vo27a08.r	AA647242 of01b11.s AW315283 12472 MAR AA622120 nq56b03.s A1801582 t091c11.x AA622570 np21f04.s	AW001308 wu28610.x AW045110 um17912.y AA552519 nk14601.s AA047528 zk73901.r	AW258184 uq31e05.y AA562591 EST7223 W54153 md17f04.r.1 AW107522 um17q12.x A1964291 EST269405 AA379625 EST92751 AA408987 EST03631	AA512284 vj19903.r AA078382 TPO2F05 C AA475410 vh17h03.r AT038272 oy85906.x AW315346 12597 WAR AA402132 zu55b03.r AA285252 PWY0756 K	ALIGNMENTS mRNA BST 18-JAN-2000 Homo sapiens cDNA clone INAGE:2668974 3' : P97805 PROTEIN EF-7;, mRNA sequence. data; Craniata; Vertebrata; Mammalia; rrhini; Hominidae; Homo. .nlm.nih.gov/ncicgap. e, Cancer Genome Anatomy Project (CGAP), ence version replaced gi:5420873. enthy.ph.D.
DB 63 31 62 80 80 50 80 83 80 80 80 80 80 80 80 80 80 80 80 80 80	417 31 AA298484 387 33 AA451058 318 33 AA451058 570 24 N41338 570 23 H26710 564 36 AA622758 564 38 AA793766 538 44 A1245950 364 49 45 AN348065 519 35 AA522348	90 90 9 30 90 9	63 35 27	33 33 33 33 33	34 33 33 33 33	Chor Cata Cata Cata Cata Cata Cata Cata Cat
Match Ler 33.5 32.4 31.8 30.5 30.4 30.0 28.4 28.4	187.6 28.0 4 167.5 28.0 4 167.5 28.0 4 157.6 28.0 4 157.6 23.6 4 157.6 23.5 5 157.6 23.5 5 144.2 21.5 5 135.8 20.3 3 126.6 18.9 4 126.6 18.9 6	18.5 18.5 18.5 18.5 18.5	17.8 17.8 17.8 17.7	17.6 17.6 17.6 16.7 16.2 16.2	16.1 15.5 15.1 14.9 14.1	AW300770 A xk05g02.x1 Similar to AW300770.1 AW300770.1 EST. Home sapien Eukaryota; Eutheria; P I (bases I NCI-CGAP bt NCI-CGAP bt NCI-CGAP bt On ational ca Tumor Gene Onpublished On Jul 8, 1 Contact: Ro
00 00 0 100 400 00	10 11 11 11 11 11 11 11 11 11 11 11 11 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		C 332 334 337 337	0 444444 00410640	RESULT 1 LOGUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL COMMENT

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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Normalized to Cot 50. Average insert size 1.32kb.
Normalized version of NCI_CGAP_Col8. Library constructed by Life Technologies."
37 a 192 c 159 g 156 t lothers
                                                                                                                             Clone distribution: NGT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW001287 668 bp mRNA EST 27-OCT-1999 wu27e06.xl Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2521282 3' similar to SW:EF07_MOUSE P97805 PROTEIN EF-7 contains MSR1.t2 MER22 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 668)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
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1 Similarity 57.5%; Pred. No. 1e-48;
181; Conservative 77; Mismatches 57; Indels
                                                                                                                                                                                                                                     Possible reversed clone: polyT not found Seq primer: -400P from Gibco High quality sequence stop: 403.
Location/Qualifiers
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, E.M., Fitzhugh, W.M., Fittchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hikle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Naughen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Otterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Rymond, L., Wai, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: MI3 Reverse.
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Other_ESTs: THC166640
Contact: Kerlavage, AR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bioinformatics
The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
713 113 1018699056
Fax: 3018699423
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                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebra!
Eutheria; Primates; Catarhini; Hominidae; Homo.
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AA297147.1 GI:1949521
EST.
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                                                                                                                                                           REFERENCE
                                                                                                                                                                                  AUTHORS
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                         VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2521282"
/clone="IMAGE:2521282"
/tissue_type="colonic mucosa from 3 patients with Crohn's disease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA297147 306 bp mRNA EST 18-APR-1997
EST112731 Colon I Homo sapiens CDNA 5' end similar to similar to
2-19 protein, mRNA sequence.
                                              Tumor Gene Index
Unpublished (1997)
On May 9, 1996 this sequence version replaced gi:1132811.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco
                              National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.5%; Score 223.8; DB 6 56.2%; Pred. No. 1.1e-48; Live 78; Mismatches 66
                                                                                                                                                                                                                                                High quality sequence stop: 478.
Location/Qualifiers
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Matches 185;
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AI883327

VERSION KEYWORDS

REFERENCE AUTHORS

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house mouse.
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Eabrafish.

Buaryota: Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

Neopterygii; Teleostei; Buteleostei; Danio.

Cyprinoidea; Cyprinidae; Rasborinae; Danio.

I (bases 1 to 770)

S Clark, M. Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R. Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Washu Zebrafish Est Project 1998

U npublished (1989)

On May 9, 1996 this sequence version replaced gi:1132813.

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-weeter: psocrait; site_l: Not1; Site_2: Sal1; lst strand cDNA was primed with a Not I - oligo(dT)15 primer | 5 prodected condection of the strand cDNA was primed with a Not I - oligo(dT)15 primer | 5 prodected condection of the stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the psPoRTI vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing.
                                                                                                                                                                                                                                              AI883327 778 bp mRNA EST 26-JUL-1999 fc60e01.yl Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to AI883327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: zbrafish@watson.wustl.edu

Chan Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resqen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
       601
                      /tissue_type="26 somite embryos, adult livers, shield stage embryos" /lab_host="XL1-blue MRF"
thggngcnaargayytnmgnggnaarwsnccnttygarcarttyytnaaraaywsnccng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www.rzpd.de)
Possible reversed clone: similarity on wrong strand
Seq primer: T3 ET from Amersham
High quality sequence stop: 467.
Location/Qualiflers
1. 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:7955"
/clone_lib="zebrafish WashU MPIMG EST"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                  AI883327.1 GI:5588491
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FEATURES

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In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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Email: Robert_Strausberg@nlh.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 aytayttygcnttyaarathtgywsnggngcngcnaaygtngtnggnccnacnatgtgyt 247
                                                                                                                                                                                                                                                                                                                                                                                                248 tygargaymgnatgathatgwsnccngtnaaraayaaygtnggnmgnggnytnaayathg 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGATGTGAATCTTCTTATCAAATTCTTGAAGAACATAGAAGATGGAAGCATTGTCATGA 548
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Unpublished (1997)
Unpublished (1997)
On Jul 28, 1997 this sequence version replaced gi:2065401.
Other ESTs: uo77804.xl
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                              DB 62; Length 778;
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                                                                                                                                                                                                                                                                                                      88; Mismatches 167; Indels
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                                                                                                                                                                                                                                           31.8%; Score 212.6; 45.6%; Pred. No. 1.2
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                                                                                                                                                                                                                                                                       Best Local Similarity 45.6*
Matches 214; Conservative
                                                                                                                         149
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Tumor Gene Index

Unpublished (1997)

On Dec 20, 1995 this sequence version replaced gi:1134301.

On Dec 20, 1995 this sequence version replaced gi:1134301.

Contact: Robert Strausbergenth.gov

Tel: (301) 496-1550

Email: Robert_Strausbergenth.gov

This clone is available royalty-free through LLNL; contact the TNAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 893 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A1936111 646 bp mRNA EST 02-SEP-1999 wo61h03.x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2459861 3'
                                                         1 (bases 1 to 615)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.4%; Score 203.2; DB 50;
58.0%; Pred. No. 3.1e-43;
iive 71; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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Best Local Similarity 58.0%
Matches 163; Conservative
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0
                                                                                                                                                                                                                                             /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, Null" 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI691072 615 bp mRNA EST 18-DEC-1999 wf22c03.xl Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351332 3' similar to SW:EF07_MOUSE P97805 PROTEIN EF-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 gnmgnggnytnaayathgcnytngtnaayggnacnacnggngcngtnytnggncaraarg 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 ACGGAACAGTAGTGCTAATGGCTACATACGATGATGGAGCAACCAAACTCACGGATGAGG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           470 snmgnaarytnttywsngayytnggnwsnwsntaygcnaarcarytnggnttymgngayw 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 cnmgntggytngcnwsnccnacnaargarathcargtnaaraartayaartgyggnytna 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 CAAAGGCGTGCCCAGAGAAGCATTTTGCTTTTAAGATGGCTAGTGGAGCAGCCAATGTCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 CAGCGGAGCTCATTGCTAAACTGGGCAGCACGTTGATCACCAGTCTTGGTATCCGAGATA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            530 sntgggtnttyathggngcnaargayytnmgnggnaarwsnccnttygarcarttyytna 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 GCTNGGTGTGTGTGTGGGAAAGACGTTAAGGAAAAGAATGGCTTTGAACAGCGGATGG 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CGCGTGGGCTGGACTCAGCCATTCGTTCTACGAAACCTCCGAGGTACAAGTGTGGGATCT
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                                                                                                                                                                                                                                                                                                                                                                                  Length 525;
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                                                                                                                                                                                                                                                                                                                                                                                                                     211;
                                                                                                                                                                                                                                                                                                                                                                                  30.5%; Score 204; DB 80; 43.2%; Pred. No. 1.7e-43;
                                                                                                                            /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:2648556"
/clone=lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sam;/dev_stage="3 months, virgin"
/lab_host="DH108"
ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                   86; Mismatches
                                                                                                               /organism="Mus musculus"
                                           Seq primer: -40RP from Gibco
High quality sequence stop: 2
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
A1691072
A1691072.1 GI:4902374
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                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                             MGI:1028978
                                                                                                                                                                                                                                                                                                                 159
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with a modified polylinker; ist strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I. - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p173 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                       COUNT LIbrary Preparation: M. Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                         Tumor Gene Index
Onpublished (1997)
On May 18, 1998 this sequence version replaced gi:3138334.
Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-1550
Email: Robert_Strausbergfaih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ayatgtaywsnggngaygtnatgcayytngtnaarttyytnaargarathccnggnggng 415
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                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 646)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="normal prostate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ww~bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:2459861"
/clone_lib="NCI_CGAP_Pr22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence stop: 438.
Location/Qualifiers
                                           AI936111.1 GI:5674981
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                                      VERSION
KEYWORDS
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                   ACCESSION
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Dietrich, N., Dubuque, T.,
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                                                                                                                                                                        vo89f11.rl Barstead mouse trradiated colon MPLRB7 Mus musculus CDN clone IMAGE:1066317 5' similar to TR:G452270 G452270 2-19 PROTEIN
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into the Not I and Eco RI sites of the modified pT7T3
vector. Library constructed by Bob Barstead, "
108 c 127 g 89 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 461)
Marray.M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuqu Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 tgcayytngtnaarttyytnaargarathccnggnggngcnytngtngtngtngcnwsnt 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="INAGE:1066317"
/clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Washu-HHMI Mouse EST Project Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1405306. Contact: Marra M.Vouse EST Project Washu-HHMI Mouse EST Project Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                   PRECURSOR. ;, mRNA sequence.
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Matches 172; Conservative
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                      345 CCCGGAGCCATT 332
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656 cnccnaarccntty
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Email: arkerlav@tigr.org
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Sadams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Milte, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wall, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Handa, M.C., Hedblom, E., Hinkle, P.S., T.,

Kelley, J.M., Kelley, J.C., Lut, L. I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Fydder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Ho, W.W., Hu, J.S., Greene, J.M., Gluber, J., Hodson, P.S., Olsen, H.,

Kaymond, L., Wei, Y.F., Ming, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, M.A., Fields, C.,

Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

AL Nature 377 (6547 Suppl.), 3-174 (1995)
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA297176 268 bp mRNA EST 18-APR-1997 EST112740 Colon I Homo sapiens CDNA 5' end similar to similar to
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aygaygayccnggnacnaaratgaaygaygarwsnmgnaarytnttywsngayytnggnw 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                        On Sep 12, 1996 this sequence version replaced gi:1288046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 3018699056
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AA297176
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Contact: Kerlavage, AR
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Fax: 3018699423
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Louistair Franches; Catarinin; Hominidae; Homo.

Louistair Franches; Catarinin; Hominidae; Homo.

Radams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Ghelm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruber, S.M.,

Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of CDNA sequence

NE Nature 377 (6547 Suppl), 3-174 (1995)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                            Gaps
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Other_ESTs: THC166640
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                                                                                                                                    Length 268;
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                              others
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                                                                                                                                         DB 31;
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EST114112 Prostate gland I Homo sapiens estimilar to 2-19 protein, mRNA sequence.
AA298484
AA298484.1 GI:1950827
                                                                                                                                    28.4%; Score 189.8; DB 3. 57.5%; Pred. No. 6.6e-40; iive 61; Mismatches 53
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                                                                                                                                                                                            Matches 154; Conservative
                            28
     ECORI;
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/db_ref="texton:10090"
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/dev_stage="4 weeks"
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/note="Organ: mammary gland; Vector: pT773D-Pac
/lab_host="DH10B"
/note="Corgan: mammary gland; Vector: pT773D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; lst strand cDNA was primed with a Not I oligo(dT) primer [5'
Site_2: Adouble-stranded cDNA was ligated to Eco RI
rgTTACCAACTGGAGGGGGGGGGGGGGGG with a Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constitucted and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA563933 518 bp mRNA EST 05-SEP-1997 nk23b02.s1 NCI_CGAP_Coll Homo sapiens cDNA clone IMAGE:1014315 3's similar to TR:6452270 6452270 2-19 PROTEIN PRECURSOR.; mRNA
     IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtnytngtngcnwsntaygaygayccnggnacnaaratgaaygaygarwsnmgnaarytn 480
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Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 518)
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                  MOI:502869
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 382.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) seq primer: MI3 Reverse.
                                                                                                                                                                Contact: Marra M.Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
                                                                                                                                                                                                                                                                                                                                                                                    247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA451058 387 bp mRNA EST 04-JUN-1997 vf86h07.rl Scares_mammary_gland_NbWMG Mus musculus cDNa clone IMAGE:850717 5' similar to TR:G452270 G452270 2-19 PROFEIN AA451058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 yinginaayggnacnacnggngcnginyi-nggncaraargcniiygayaigiaywsngg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1394413
                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                        DB 31; Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 ngaygtna-tgcayytngtnaarttyytnaargarathccnggnggngc 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :|| | ||||::| || |||:|| 368 AGGIGTTATTGCACCTAGTGAAATINCTTAAAGAAATTCCCGGGGGGGG 416
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                  Query Match 28.0%; Score 187.6; DB 31; Best Local Similarity 62.6%; Pred. No. 3.3e-39; Matches 181; Conservative 56; Mismatches 50;
                                                                                                      /organism="Homo sapiens"
/db_xref="ATCC (inhost):175003"
/db_xref="taxon:9606"
/clone_lib="Prostate gland I"
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA451058.1 GI:2164728
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JOURNAL
COMMENT
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KEYWORDS
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This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408 nggnggngcnytngtnytngtngcnwsntaygaygayccnggnacnaaratgaaygayga 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 GCCTTCTGACATGTGGGCCGGAGATGTCAACGACCTGTTGAAGTTTATT-CGGCCACTGA 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              528 ywsntgggtnttyathggngcnaargayytnmgnggnaarwsnccnttygarcarttyyt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Washu-Merck EST Project
Unpublished (1995)
On May 8, 1995 this sequence version replaced gi:801446.
Contact: Wilson RK
Washington University School of Medicine
   Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P.
                                                                                                                                                 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.6%; Score 157.6; DB 2
48.4%; Pred. No. 2.9e-31;
ive 69; Mismatches 92
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                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="GDB:3887042"
/db_xref="taxon:9606"
                                                                                                                                                                                                                               High quality sequence stops: 331
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 331
Location/Qualifiers
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                                                          TITLE
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                                                                                                                                                 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GSP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: colon; Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Multiple colon tumors. 5' adaptor sequence: 5' GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yw68g05.rl Soares_placenta_8to9weeks_2NbHP8tc9W Homo sapiens cDNA
clone IMAGE:257432 5', mRNA sequence.
N41338
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 acnaaratgaaygaygarwsnmgnaarytnttywsngayytnggnwsnwsntaygcnaar 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           511 carytnggnttymgngaywsntgggtnttyathggngcnaargayytnmgnggnaarwsn 570
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 410)
H1111er,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
HOlman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JAN-1996
                                     Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1290555.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.1%; Score 161.4; DB 35; Length 518; 58.0%; Pred. No. 3.3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Inbas:1014315"
/clone_lib="NCI_CGAP_CO11"
/tissue_type="tumor"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 CTGCTGGAGATGGAGGCCTGCATGCCCCCGAAGCCATTT 300
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                                                                                                                                                                                                                                                                                                                          Insert Length: 650 Std Error: 0.00 Seq primer: -40ml3 fwd. Er from Amersham High quality sequence stop: 452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Mismatches
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N41338
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335 tnytnggncaraargcnttygayatgtaywsnggngaygtnatgcayytngtnaarttyy 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H26710
H26710.1 GI:896700
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                                                                                                                                                                                                                       455 aratgaaygaygar 468
                                                                                                                                                                                                                                                                      554 AGATGAATGACGAG 567
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/dev_stage="adult"
/lab_host="badult"
/lab_host="badult"
/lab_host="badult"
/note="vector: pWE18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGCTAATGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector [5' site CACTGTGTG, 3' site
CACATGTG). XhoI should be used to isolate the CDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sunio Sugano
(University of Tokyo Institute of Medical Science) and
kindly donated by Dr. Koichi Kawakami. Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCACAA.

118 c 153 g 155 t
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Repterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinidae; Rasborinae; Danio.

1. (Dases 1 to 570)

Sugano, S., Kawakami, K., Johnson, S., Li,F., Marra, M., Eddy, S., Hillier, L., Cilfton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, T., Martin, J., Pape, D., Steptoe, M., Underwood, K., Theising, B., Martin, J., Pape, D., Steptoe, M., Underwood, K., Theising, B., Ritter, E., Bowers, Y., Wylle, T., Waterston, R. and Wilson, R. Washu Zobrafish Est Project 1999

On Jun 22, 1998 this sequence version replaced gi:3246857.

Contact: S.L. Johnson

Washington University School of Medicine

Washington University School of Medicine

Washington Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by: Washington University Genome Sequencing Center Seq primer: T3 Er from Amersham High quality sequence stop: 523.
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f135h03.yl Sugano Kawakami zebrafish DRA Danio rerio cDNA clone 2639669 5' similar to SW:G786_HUWAN Q92520 PROTEIN GS3786. ;contains THR.t3 THR repetitive element ;, mRNA sequence.
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/db_xref="taxon:7955"
/clone="2539669"
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/sex="mixed (one male and one female, including unfertilized eggs)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
                                                                      AW175415
AW175415.1 GI:6441452
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Fax: 314 286 1810
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KEYWORDS
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                                                            454
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1 (bases 1 to 376 Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hollman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikfuh, L., Rohlfing, T., Soares, M., Tan, F., Treyaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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395 tnaargarathconggnggngonytngtnytngtngcnwsntaygaygayconggnaona
                                                                                      H26710 376 bp mRNA EST 12-JUL-
yl14b12.rl Soares breast 2NbHBst Homo sapiens CDNA clone
IMAGE:158207 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Best Local Similarity 46.4%; Pred. No. 1.7e-30;
Matches 166; Conservative 75; Mismatches 115;
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Search completed: May 31, 2000, 17:51:19 Job time: 3436 sec

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APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Colon Specific Genes and Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Carella, Byrne, Bain, Gilfillan, Cecchi,
E: Stewart & Olstein
6 Becker Farm Road
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STATE:

OUNTRY:

IN O7068-1739

COMPUTER READABLE FORM:

MEDTIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,667

FILING DATE:

FILING DATE:

NAME: Ferrancy, Gregory D.

REGISTRATION NUMBER: 35,134

REGISTRATION NUMBER: 35,134

REFERENC/POCKET NUMBER: 325,00-435

TELEPHONE: 201-994-1740

TELEPHONE: 201-994-1744

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:

LENTH: 548 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
US-08-469-277-1
US-08-466-1
US-08-486-946-1
US-08-808-641-2
US-09-915-438-2
US-09-915-438-2
US-08-853-659A-11
US-08-853-659A-8
US-08-853-659A-8
US-08-853-659A-8
US-08-853-659A-6
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CITY: Roseland
STATE: NJ
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       May 31, 2000, 19:14:15 ; Search time 57.43 Seconds (without alignments) 1514.191 Million cell updates/sec
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7: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
                                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 548;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.0%; Score 294.6; DB 6;
59.3%; Pred. No. 2.4e-80;
11ve 93; Mismatches 72;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP 91 114 300.6
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ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite
CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                              Query Match
Best Local Similarity 59.3%
Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BENT, Stephen A.
                                                                       mat_peptide
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: APPLICATION NUMBER:
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                 ; LOCATION:
; FEATURE:
; NAME/KEY:
; LOCATION:
PCT-US95-07289-6
              LOCATION:
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                                                                                         265 atgwsnccngtnaaraayaaygtnggnmgnggnytnaayathgcnytngtnaayggnacn 324
                                                                                                                       Gaps
                                      Indels
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GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Colon Specific Genes and Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         congarytnytngaratggarggntgyatgconconaarcontty 669
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ADDRESSE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
COUNTRY: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Elopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07289
FILING DATE: 06-JUN-1995
CLASSIFICATION:
NAME: Ferraro, Gregory D.
REGISTRATION:
NAME: FERRENCE/DOCKET NUMBER: 325800-265
TELECOMMUNICATION:
  59.3%; Pred. No. 2.4e-80;
cive 93; Mismatches 72;
Best Local Similarity 59.38
Matches 240; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
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PCT-US95-07289-6
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                                                                                                                                                                                                                                                                  Query Match 7.3%; Score 48.6; DB 1; Length 7218; Best Local Similarity 9.9%; Pred. No. 0.00025; Matches 42; Conservative 169; Mismatches 214; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Coats, Steven R.
APPLICANT: Bass, Michael B.
APPLICANT: Bass, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5973119el Cyclin E Genes and Proteins FILE REFERENCE: A-524
CURRENT APPLICATION NUMBER: US/09/092,770
CURRENT FILING DATE: 1997-06-05
NUMBER OF SEQ ID NOS: 18
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09092770 Patent No. 5973119 GENERAL INFORMATION:
                                                                                 TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                         REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                            ; TOPOLOGY: linear; IMMEDIATE SOURCE: CLONE: pTZgpt-Fls US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Human
US-09-092-770-8
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LENGIH: 1215
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94 aaracnathmgnytnccnmgntggytngcnwsnccnacnaargarathcargtnaaraar 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454 CYTCNARNARCCARTCNARNARDAINSWNCKCATYTGNGGYTCNARRTCNSWRIGNARNA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 CYTCRAARTGYTTRTCRTGNACRTANCKNSWYTCYTTYTNARCATRTTNARCCANACYT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 ytnggnttymgngaywsntgggtnttyathggngcnaargayytnmgnggnaarwsnccn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   574 ttygarcarttyytnaaraaywsnccngayacnaayaartaygarggntggccngarytn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 ytnaargarathccnggnggngcnytngtnytngtngcnwsntaygaygayccnggnacn
             Length 1215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APPLICANT: Mitthuln, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-10S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,241
ch 5.9%; Score 39.4; DB 4; 1 Similarity 9.0%; Pred. No. 0.033; 52; Conservative 169; Mismatches 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             634 ytngaratggarggntgyatgconconaarcontty 669
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STREET: 1 South Pinckney Street
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COMPUTER READABLE FORM:
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; LOCATION:
US-08-922-182-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 naaygtngtnggnccnacnatgtgyttygargaymgnatgathatgwsnccngtnaaraa 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 yaaygtnggnmgnggnytnaayathgcnytngtnaayggnacnacnggngcngtnytngg 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 hmgnytnccnmgntggytngcnwsnccnacnaargarathcargtnaaraartayaartg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 CGCCGACCGGCTCGAGACCGCTCTGGCCCGGGCTGGACCTGCAGCCGGCGTTCGATGTGGT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 ncaraargenttygayatgtaywsnggngaygtnatgcayytngtnaarttyytnaarga 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.4%; Score 35.8; DB 2; Length 1058; 27.3%; Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08922182;
Patent No. 5834300
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Barber, Robert D
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Mismatches 201; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rathccnggnggngcnytngtnytngtngcnwsntaygayg 442
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, NICholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93511
TELECOMMUNICATION INFORMATION:
TELEFAX: 608-251-500
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1058 base pairs
                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Rhodobacter sphaeroides
STRAIN: 2.4.1
IMMEDIATE SOURCE:
CLONE: pUI8017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 27.38 Matches 93; Conservative
                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 221..895
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CITY: Ma.
STATE: WI
COUNTRY: US
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US-08-922-182-3
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102 hmgnytnccnmgntggytngcnwsnccnacnaargarathcargtnaaraartayaartg 161
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          COMPUTER: LOCATION COMPATION OF SELECTION NUMBER: US/08/922,182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
5.4%; Score 35.8; DB 3;
Best Local Similarity 27.3%; Pred. No. 0.36;
Matches 93; Conservative 47; Mismatches 201;
                                                                                                                                                                                                                                                                                              NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93511
TELECOMMUICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodobacter sphaeroides
                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08919953
Patent No. 5837481
GENERAL INFORMATION:
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Barber, Robert D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISICS:
Floppy disk
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1058 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                               FILING DATE
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APPLICANT:
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541 athggngcnaargayytnmgnggnaarwsnccnttygarcarttyytnaaraaywsnccn 600
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GENERAL INFORMATION:
APPLICANT: Rosenblum, Michael
APPLICANT: Kohr, William Jack
APPLICANT: APPLICANT: APPLICANT: Protein Structure of the Plant Toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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601 gayacnaayaartaygarggntggccngarytnytngaratgga
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                                                                                                      US-08-674-887A-5

Sequence 5, Application US/08674887A

Patent No. 5939300

GENERAL INFORMATION:
APPLICANT: Robertson, Dan E.
APPLICANT: Adhiwari, Robert S.
TITLE OF INVENTION:
CATALASES

NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: TBM COMPALIBLE
COMPUTER: TBM COMPALIBLE
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 41.3%; Pred. No. 0.94
Matches 43; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09015/002001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION UNDRER: 38,347
REPERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Coding Sequence;
COCATION: 1...2259
US-08-674-887A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2262 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                      STREET: 4222
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 92037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 CGCCGACCGGCTCGAGACCGCTCTGGCCCGGCTCGACCTGCAGCCGGCGTTCGATGTGGT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 hmgnytnccnmgntggytngcnwsnccnacnaargarathcargtnaaraartayaartg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 CCTTTGGCCGGGTTATCGCGTCAGGCGGATGTGCTAGCCTCGTGAAAAGACGTATGGGAC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 yggnytnathaarccntgyccngcnaaytayttygcnttyaarathtgywsnggngcngc 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 CTTCTGCGATGCGCTGTCGATGACGCTCCAAGGCGGTGGCGGGACTGACCCACATCGAATC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 yaaygtnggnmgnggnytnaayathgcnytngtnaayggnacnacnggngcngtnytngg 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 ncaraargcnttygayatgtaywsnggngaygtnatgcayytngtnaarttyytnaarga 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 GGTGCTGGATCTGAACCTGCCGGACGTGAACGCCCTCGACGGCCTCATCCGTCTGAAGGC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.4%; Score 35.8; DB 3; Length 1058; 27.3%; Pred. No. 0.36; tive 47; Mismatches 201; Indels 0
                TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE TITLE OF INVENTION: SENSING AND REMEDIATION UNMER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rathccnggnggngcnytngtnytngtngcnwsntaygayg 442
                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,953
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 960296.93511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: Rhodobacter sphaeroides 2.4.1
                                                                                                        ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1058 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93; Conservative
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 221..895
US-08-919-953-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN: 2.4.1
IMMEDIATE SOURCE:
CLONE: pUI8017
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                                                                                                                                                                                                                     53703
                                                                                                                                                                             STATE: WI
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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322 acnacnggngcngtnytnggncaraargcnttygayatgtaywsnggngaygtnatgcay 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 ytngtnaarttyytnaargarathconggnggngcnytngtnytngtngcnwsntaygay 441
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APPLICANT: Grun Ph.D., Felix
APPLICANT: Buck Ph.D., Jochen
APPLICANT: Hammerling Ph.D., Ulrich
TITLE OF INVENTION: ISOLATION, PURIFICATION AND CLONING OF
TITLE OF SEQUENCES: 2
CORRESPONENCE ADDRESS:
ADDRESSEE: MIXON, HATGRAVE, DEVANS & DOYLE-LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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5.3%; Score 35.2; DB 4;
Best Local Similarity 36.1%; Pred. No. 0.78;
Matches 53; Conservative 19; Mismatches 75;
                               540 yathggngcnaargayytnmgnggnaarws 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 1963/771
TELECOMMUNICATION INFORMATION:
TELEFHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,178
FILING DATE: 09-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               442 gayccnggnacnaaratgaaygaygar 468
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                                                                            31 CYTTNGTNSWRAANSWNACNGTRTCNARNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/852,481
                                                                                                                                                                                                            ; Sequence 1, Application US/08852481
; Patent No. 5928931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/08868786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1564 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : New York
RY: U.S.A.
14603
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                            RESULT 10
US-08-852-481-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 nttywsngayytnggnwsnwsntaygcnaarcarytnggnttymgngaywsntgggtntt 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 CNGGNGCRTCYTTRAARAARTANSWNCKRTTNCKNACYTGRTANCCNACNACRTANACNS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ngtnytngtngcnwsntaygaygayccnggnacnaaratgaaygaygarwsnmgnaaryt 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 CRAARCAYTINCCNGGRICRICNCCYTINSWNARNARNGGDAINCCRIGNSWRIINCCYI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNGGYTTNARYTTNACNCKNARYTCRTTNARRAARTTNACRTANGTDATRTANGTNGCNC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.3%; Score 35.2; DB 6; Length 774; Best Local Similarity 16.2%; Pred. No. 0.42; Matches 63; Conservative 75; Mismatches 252; Indels
                                                                                                                                                                                         COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

APPLICATION NUMBER: PCT/US91/05766

FILING DATE: 19910814
                                                                       ADDRESSEE: Fulbright & Jaworski Patent Department
STREET: 1301 McKinney #5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Launer, Charlene A.
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: D-5195 PCT
TELECOMNUNICATION INFORMATION:
TELEPHONE: (713)651-5246
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 Dasse pairs
LENGTH: 774 Dasse pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/567,220
FILING DATE: 14-AUG-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Gelonium multiforum
DEVELOPMENTAL STAGE: Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
ORIGINAL SOURCE:
TITLE OF INVENTION: Gelonin
                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: 1..774 PCT-US91-05766-1
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                            CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
                                                                                                                                                                               COUNTRY: USA
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NUMBER OF SEQUENCES:

NUMBER OF SEQUENCES:

ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: n c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 gcnttyaarathtgywsnggngcngcnaaygtngtnggnccnacnatgtgyttygargay 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 aayggnacnacnggngcngtnytnggncaraargcnttygayatgtaywsnggngaygtn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.2%; Score 35; DB 4; Length 2855; Best Local Similarity 31.4%; Pred. No. 1.5; Matches 77; Conservative 30; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/852,153
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guth, Joseph H.
REGISTRATION NUMBER: 1224.006
TELECOMMUNICATION NUMBER: 1224.006
TELECOMMUNICATION NUMBER: 1224.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-3888
TELEPHONE: (510) 923-3888
TELEPHONE: (510) 655-354.2
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2855 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
2160 TAAATATCTTCGGCATCGTTTAT 2182
                                                                                                          US-08-852-153-1/c

Sequence 1, Application US/08852153
Patent No. 5914266
GENERAL INFORMATION:
APPLICANT: Randazzo, Filippo
TITLE OF INVENTION: Mammalian Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-852-153-5/c; Sequence 5, Application US/08852153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (genomic) US-08-852-153-1
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: Sil
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1127 CTGCA 1123
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                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 94608
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APPLICANT: Kawchuk, Lawrence M.
APPLICANT: Armstrong, John
APPLICANT: Lynch, Dermot
APPLICANT: Lynch, Dermot
APPLICANT: Knowles, Richard
APPLICANT: Fortatoes Having Improved Quality
TITLE OF INVENTION: Characteristics and Methods for Their Production
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 tnytngtngcnwsntaygaygayccnggnacnaaratgaaygaygarwsnmgnaarytnt 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 aywsnggngaygtnatgcayytngtnaarttyytnaargarathccnggnggngcnytng 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868,786
FILING DATE: 04-JUN-1997
CLASSIFICATION NUMBER: US 60/036,946
FILING DATE: 10-FBB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sullivan, Sally A
REGISTRATION NUMBER: 8-97
REGISTRATION NUMBER: 8-97
RELECOMMUNICATION NUMBER: 8-97
TELEPHONE: (303) 499-8080
TELEPHONE: (303) 499-8080
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENERAL (3103) 499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 44..2944
OTHER INFORMATION: /product= "potato alpha-glucan OTHER INFORMATION: L-type tuber phosphorylase"
                                                                                                                                                                                                                            E: Greenlee, Winner and Sullivan, P.C. 5730 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482 tywsngayytnggnwsnwsntay 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3101 base pairs
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194..2941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSEE: Greenlee,
                                                                                                                                                                                                                                                                       CITY: Boulder
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                80803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION:
US-08-868-786-1
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Query Match
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APPLICANT: Randazzo, Filippo
TITLE OF INVENTION: Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                        Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1767 GAGTGACAAGTGAGTCTGTGTAAAGGGCTGGTTGCCAAACAGATTGTCACTACGAAGGTT 1708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 garathcargtnaaraartayaartgyggnytnathaarccntgyccngcnaaytaytty 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.2%; Score 35; DB 4; Length 3255; Best Local Similarity 31.4%; Pred. No. 1.7; Matches 77; Conservative 30; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,153
                                                                                                                                                     STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASALECATION: 4.3.
ATTORNEY/ACENT INFORMATION:
NAME: Guth, JOSEPH H.
REGISTRATION UNDERE: 31,261
REFERENCE/POCKET NUMBER: 1224
TELECOMMUNICATION INFORMATION:
TELEFAM: (510) 655-3542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3255 base pairs
TYRE: nucleic acid
STRANDENESS: single
                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08852153
Patent No. 5914266
                                                APPLICANT: Randazzo, Filippo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                              TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
Patent No. 5914266
GENERAL INFORMATION:
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US-08-852-153-3/c
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1839 GAGIGACAAGTGAGTCTGTAAAGGGCTGGTTGCCAAACAGATTGTCACTACGAAGGTT 1780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zain, Sayeeda
APPLICANT: Lukanidin, Engene
TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
TITLE OF INVENTION: THE MTS-1 GENE
CORRESPONDENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City STATE: New York STATE: New York COUNTRY: United States II530
                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guth, Joseph H.
REGISTRATION NUMBER: 31,261
REFERENCE/DOCKET NUMBER: 1224
TELECOMMUNICATION INFORMATION:
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3327 Dase pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08190560; Patent No. 5798257; GENERAL INFORMATION:
                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-852-153-3
                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                         Emeryville
California
                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                               U.S.A.
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                                                                                                        94608
                                                                               COUNTRY:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
COMPUTER: IBM C Compatible
COMPUTER: IBM C COMPA:-
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
FILING DATA:
APPLICATION NUMBER: US/08/190,560
FILING DATE:
CLASSIFLATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Didigilo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 7879ZY
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4366
TELENTH: 579 base pairs
TYPRE: nucleic acid
STRANDEDENESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-190-560-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        590 araaywsnccngayacnaa 608
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Search completed: May 31, 2000, 19:14:25 Job time: 6263 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

May 31, 2000, 19:03:54 ; Search time 78.65 Seconds (without alignments) 2128.144 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-186-342-8 669 1 atgmgngtnwsnggngtnyt.....gyatgccnccnaarccntty 669

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

311585 seqs, 125096042 residues Searched:

623170 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

N_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Consensus sequence	Full length sequen	Human colon specif	Polynucleotide seq	Clone 1281865 EST	Clone 1735382 EST			-	DNA fragment contg	Staphylococcus aur	Human secreted pro	Xylanase xynB gene	Human interleukin-	Human SOX-9 cDNA.	Staphylococcus aur	Continuation (10 o	R. sphaeroides Adh	Rhodobacter sphaer	Interferon-beta ge	Staphylococcus aur	Brevibacterium fla	Alcaligenes (Deley	Solanum tuberosum	Staphylococcus aur	DNA encoding a Sta	ď	Human sex comb on						
CHANGE	Œ		V63516	V63515	T45883	V16671	V63509	V63511	V63510	V63508	V63512	N70938	V74910	V69614	T08144	V31480	T30309		V21209_09	V62126	V64113	N20057	V74828	T29734	V06554	V32918	V77877	T83899	V53367	V00011	T97297	T97299	V00013	T97298	0	
	DB.	;	Н	Н	Н	Н		Н	٦	Н	П	Н		Н	н	-	Н	Н	-1			Н	Н	Н	Н	Н	-	H	7	٦	Н	П	Н	H	7	,
		- 1	1299	955	548	548	263	251	228	287	187	3830	704	1341	1633	687	3934	8536	110000	1058	1058	1836	4544	1836	2262	3101	420	1442	1442	2855	2855	3255	3255	3327	3327	010
di	Query Match Length		ζ.	8.99	4	4	θ.	27.1	4				5.7				5.5	5.4	5.4						5.3					•					5.5	
	Score		485.8	447	294.6	294.6	193.6	181.4	161.8	59.2	40.4	39	37.8	37	36.8	36.6	36.6	36.4	36.4	35.8	2	35.6	S	35.4	ū.	5	35	35	35	35	35	35	35		35	
	Result		п	7	ю	4	ស	9	7	80	6	10	11	c 12	13	14		c 16		18	19	c 20	21	22	23	24	25	26	27						c 33	

Human gene signatu	EST CLONE JOSS. NE Human nuclear prot	Nucleotide sequenc	Enterococcus faeca	Bettle patched gen	Tribolium castaneu	Tribolium casteneu	ACC oxidase GEFE-1	Borrelia burgdorfe	Chrysanthemum flav
T20500	V86183 V38564	V68588	X12987	T14225	V21586	V64098	T66248	X20271	T94661
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5.2	5.2	5.5	5.2	5.1	5.1	5.1	5.1	5.1	5.1
34.8	34.8 34.8	34.8	34.6	34.4	34.4	34.4	34.4	34.4	34.2
35	37	38	39	40	41	42	43	44	45
				υ	O	υ			c)

ALIGNMENTS

MESULT 1 V63516 standard; CDNN, 1299 BP. To 36356; Master antry) E Consensus sequence of CSIA1 ESTSence. E ST sequence; CSIA1; gastrointestinal tract; cancer; Barret's esophagus; Mastric ulocer; gastritis; leicomyoma; polyps; Crohn's disease; consensus sequence of CSIA1 ESTSence. EST sequence; CSIA1; gastrointestinal tract; cancer; Barret's esophagus; Mulcerative colitis; Pantreatitis; ss. EST sequence; CSIA1; gastrointestinal tract; cancer; Barret's esophagus; Mulcerative colitis; Pantreatitis; SST sequence of CSIA1 Pantreatitis; PR 37 Pantreatitis EN WOB44133-A1. PR 37 MARD JABOTT LAB WOB44133-A1. PR 37 MARD JABOTT LAB MARD JABOTT	Oy 121 gcnwsnccnacnaargarathcargtnaaraartayaartgyggnytnathaarccntgy 180
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BP;

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Sequence

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28-JAN. 1999 (first entry)
Full length sequence of clone 1281865 corresponding to CS141 sequence.
EST sequence; CS141; gastrointestinal tract; cancer; Barret's esophagus; gastric ulcer; gastritis; lelomyoma; polyps; Crohn's disease; ulcerative colitis; pantreatitis; ss.
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                                                                                                                        atgtgyttygargaymgnatgathatgwsnccngtnaaraayaaygtnggnmgnggnytn
   congcnaaytayttygcnttyaarathtgywsnggngcngcnaaygtngtnggnccnacn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABBO ) ABBOTT LAB
Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR,
Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;
WPI; 98-568280/48
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31-MAR-1998; U06337.
31-MAR-1997; US-828489.
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WO9844133-A1.
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Claim 1; Page
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Colon specific gene; CSG4; colon cancer; metastasis; diagnosis; gene therapy; ss.
Homo sapiens.
                          Length
                         447; DB 1; Le
No. 5.8e-119;
Smatches 103;
ij.
                                           Conservative 141; Mismatches
                          Score
Pred.
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                         66.8%;
60.0%;
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13-MAR-1997 (first entry)
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06-JUN-1995; U07289.
06-JUN-1995; WO-U07289.
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                                  Similarity
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WPI; 97-043054/04.
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08-OCT-1998.
31-MAR-1998; U06337.
31-MAR-1997; US-828489.
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WO9844133-A1.
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of which, in non-colon tissue samples, can be used as indication of colon cancer metastasis

Slaim 1: Fig 4: 60pp; English.

13 CDNA clones (74580-92), most of them partial clones, correspond to human colon specific genes, designated CSG1, CSG2, etc., that creaming the primarily expressed in tissues derived from the colon. CSG7 and CSG10 show reduced expression in colon cancer cells as compared to that in normal cells; the remaining genes are overexpressed in colon cancer. The partial cDNA sequences can be used to isolate full-length clones and genomic clones including the complete gene.

CSG nucleic acids can be used to produce CSG polypeptides (see also w06545-53) in transformed host cells, as probes to detect disorders of the colon, partic. colon cancer and colon cancer metastasis, and
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                                                                                                                                                                                                                    DB 1; Length 548;
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Polynucleotide sequence of a colon-specific gene.
Colon-specific gene; probe; detection; expression; human; diagnostic assay; colon cancer; antibody; screening; ss.
                                                                                                                                                                                                                44.0%; Score 294.6; DB 1; Length 59.3%; Pred. No. 2.8e-75; Indels iive 93; Mismatches 72; Indels
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Claim 15; Fig 4; 51pp; English
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                                                                                                                                                                            137 A;
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06-JUN 11995; 469667.
06-JUN 11995; US-469667.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                             Local Similarity 5.3.3 les 240; Conservative
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WPI; 98-229823/20.
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EST sequence; CS141; gastrointestinal tract; cancer; Barret's esophagus; gastric ulcer; gastritis; lelomyoma; polyps; Crohn's disease; ulcerative colitis; pantreatitis; ss.
           full-length
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V16668-81 represent polynucleotide sequences of partial or full-lengt cDNA clones of colon-specific genes. The polynucleotides can be used as probes to detect expression of the corresponding human genes, e.g. diagnostic assays for detecting micrometastases of colon cancer. Recombinant cells containing the polynucleotides can be used to produce the polypeptides, in order that antibodies can be raised and used in further screening or diagnostics. 173 G; 107 T;
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V63504-15 represent a set of contiguous and partially overlapping Essequences designated CS141. The sequences are isolated from a cDNA library made from gastrointestinal tract tumour and normal tissues. The CS141 gene is useful as a marker for gastrointestinal tract disorders. The methods and products can be used in detecting,
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Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;
WPI; 98-568280/48.
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Pred. No. 2.8e-75;
3; Mismatches 72;
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Clone 1753382 EST corresponding to CS141 sequence.
Clone 1753382 CS141; gastrointestinal tract; cancer; Barret's esophagus; gastric ulcer; gastriits; lelomyoma; polyps; Crohn's disease; ulcerative colitis; pantreatitis; ss.
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Claim 1; Page 91; 116pp; English.
V63504-15 represent a set of contiguous and partially overlapping EST sequences designated CS141. The sequences are isolated from a CDNA library made from gastrointestinal tract tumnour and normal tissues.
The CS141 gene is useful as a marker for gastrointestinal tract disorders. The methods and products can be used in detecting, disponsing, staging, monitoring, prognosticating, preventing, or determining the predisposition to diseases and conditions of the gastrointestinal tract, such as gastrointestinal tract cancers, Barret's esophagus, gastric coller, gastritis, leiomyoma, polyps, crohn's disease, ulcerative collis, 7f R:
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diagnosing, staging, monitoring, prognosticating, preventing, or determining the predisposition to diseases and conditions of the gastrointestinal tract, such as gastrointestinal tract cancers, Barret's esophagus, gastric ulcer, gastritis, lelomyoma, polyps, Crohn's disease, ulcerative colitis, pantreatitis. Sequence 263 BP; 69 A; 70 C; 66 G; 58 T;
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Salling-Wedel PA. Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR Kratochvil JD, Roberts-Rapp L, Russell TC Ctroums
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61.2%; Pred. No. 1.8e-46;
11ve 59; Mismatches 43
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31-MAR-1998; U06337.
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EST sequence, CS141; gastrointestinal tract; cancer; Barret's gastric ulcer; gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis; pantreatitis; ss.
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43;
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58.1%; Pred. No. 2.4e-37;
ive 51; Mismatches 44;
Mismatches
63;
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Best Local Similarity 58.1%
Matches 132; Conservative
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31-MAR-1998; U06337.
31-MAR-1997; US-828489.
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Length 251;

Score 181.4; DB 1; Pred. No. 5.8e-43;

27.1%; 57.6%;

Query Match Best Local Similarity

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Claim 1; Pages 91-92; 116pp; English.
V63504-15 represent a set of contiguous and partially overlapping EST sequences designated CS141. The sequences are isolated from a cDNA library made from gastrointestinal tract tumour and normal tissues. The CS141 gene is useful as a marker for gastrointestinal tract disorders. The methods and products can be used in detecting, disonosing, staging, monitoring, prognosticating, preventing, or determining the predisposition to diseases and conditions of the gastrointestinal tract, such as gastrointestinal tract cancers, Barret's esophagus, gastric ulcer, gastrointestinal tract cancers, Crohn's disease, ulcerative collits, pantreathis; leiomyoma, polyps, Crohn's disease, ulcerative collits, pantreathis; leiomyoma, polyps, Sequence 187 BP; 35 A; 42 C; 74 G; 33 T;
                                                                                                              wew gastrointestinal tract specific polynucleotides, CS141 - used develop products for the diagnosis and treatment of e.g. cancers, gastric ulcer, gastritis, Crohn's disease, ulcerative colitis or parcreatitis
                                  (ABBO ) ABBOTT LAB.
Billing-Wedel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR, Kratcchvil JD, Roberts-Rapp L, Russell JC, Stroupe SD; WPI; 98-568280/48.
                      31-MAR-1997; US-828489.
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      31-MAR-1998; U06337
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20-NOV-1986; J00596.
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EST sequence; CS141; gastrointestinal tract; cancer; Barret's esophagus; gastric ulcer; gastritis; lelomyoma; polyps; Crohn's disease; ulcerative colitis; pantreatitis; ss.
                                                                                                                                                                                                                                                      Barret's esophagus;
                   V63504-15 represent a set of contiguous and partially overlapping EST sequences designated CS141. The sequences are isolated from a cDNA library made from gastrointestinal tract tumour and normal tissues. The CS141 gene is useful as a marker for gastrointestinal tract disorders. The methods and products can be used in detecting, diagnosing, staging, monitoring, prognosticating, preventing, or determining the predisposition to diseases and conditions of the
394 ytnaargarathccnggnggngcnytngtnytngtngcnwsntaygaygayccnggnacn 453
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                                                                                                                                                                                                                                                                                                                                              131-MAR-1998; U06337.

31-MAR-1999; U06337.

31-MAR-1997; US-288489.

(ABBO ) ABBOTT LAB.

Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR,
Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;
WPI; 98-568280/48

New gastrointestinal tract specific polynucleotides, CS141 - used develop products for the diagnosis and treatment of e.g. cancers, gastric ulcer, gastritis, Crohn's disease, ulcerative colitis or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrointestinal tract, such as gastrointestinal tract cancers, Barret's esophagus, gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative colitis, pantreatitis. Sequence 287 Bp; 54 A; 85 C; 87 G; 58 T;
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EST sequence; CS141; gastrointestinal tract; cancer; Barret's gastric ulcer; gastritis; leiomyoma; polyps; Crohn's disease; Synthetic.
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                                                                  aaratgaaygarwsnmgnaarytnttywsngayytnggnwsnws 500
                                                                                  DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 90; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V63512 standard; cDNA; 187 BP.
                                                                                                                                                                                V63508 standard; cDNA; 287
                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                   Homo sapiens.
WO9844133-A1.
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WO9844133-Al.
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Best Local S
Matches 49,
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V63508
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                                                         Gaps
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                                                                                                                                                                                                                                                                                                                  10-APR-1991 (first entry)
DNA fragment contg. streptomycin resistance gene and its regulatory sequence from Streptomyces griseus 4-1 strain (FERM BP-1198).
Antibiotic-resistance; selection marker; ss.
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The DNA fragment can be inserted into an actinomycetes plasmid vector (e.g. pIJ720) to give a hybrid plasmid which may be used streptomycin resistance selection marker.

Sequence 3830 BP; 576 A; 1367 C; 1348 G; 538 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA contg. streptomycin resistance gene and regulatory sequence useful as resistance selection marker, isolated from plasmid pST141 Streptomyces lividans 4-1
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                                                                                                     699
6.0%; Score 40.4; DB 1; Length 187; 67.3%; Pred. No. 0.018;
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                                                                                                  618 rggntggccngarytnytngaratggarggntgyatgccnccnaarccntty
                                                                                                                            8; Indels
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                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-NOV-1985; JP-258622.
(ZAID) ZH BISEBUTSU KAGAKU KEN.
(UMEZ/) UMEZAWA H.
UMEZAWA H. IKAMI Y;
                                                                                                                                                                                                                                                                         N70938 standard; DNA; 3830 BP.
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/*tag= a
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                       Best_Local Similarity 67.3
Matches 35; Conservative
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Matches
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WPI; 37-31422/35.

WPI; 37-31422/35.

Torond on computer readable medium and used in the production of anti-S.aureus vaccines
anti-S.aureus vaccines

Claim 1; Page 1531-1532; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used contrained on the community readable.

Communion readable medium surgicals a primers or probes for isolating communion readable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
361. 420
/*tag= a
/*note= "these bases represent a line of missing text in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
AGAGGCGTTCATCTTCGCGGTGAAGTCCAACGTCACCGCACGGACTGCCGTCTCCCTCGA 136
                                                                                                                                                 naayggnacnacnggngcngtnytnggncaraargcnttygayatgtaywsnggngaygt 374
                                                                                                                        natgcayytngtnaarttyytnaargarathccnggnggngcnytngtngtngcnws 434
                                                                                                                                                                                                 ntaygaygayccnggnacnaaratgaaygaygarwsnmgnaarytnttywsngayytngg 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus contig SEQ ID #599.
                                                                                                                                                                                                                                                                           524
                                                                                                                                                                                                                                                                                                             317 CCCCACCGAGGGGGGGGAAGCTGGCGAGCCG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΰ
                                                                                                                                                                                                                                                                           nwsnwsntaygcnaarcarytnggnttymg
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                                                                                                                                                                                                                                                                                                                                                                                                       V74910 standard; DNA; 704 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97-374922/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                          V74910;
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                 77
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Length 704;

Score 37.8; DB 1; Pred. No. 0.28;

5.7%;

Query Match Best Local Similarity

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Claim 4; Page 104; 142pp; English.
Claim 4; Page 104; 142pp; English.
Claim 4; Page 104; 142pp; English.
This sequence represents a nucleic acid molecule designated Gene 4 from the separate of the page 104; 142pp; English and Proceed as corrected human protein. This gene maps to chromosome 4 and is abundantly expressed in parathyroid tumour. It is useful for diagnosis and treatment of disorders of the nervous system and the protein products are useful in modulating calcium metabolism.
The invention relates to 20 novel genes and their fragments (V69611 to V69630) and corresponding secreted proteins (W83931 to W83950) which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein gene 4 clone HEBND56.
Secreted protein; gene therapy; protein therapy; diagnosis; treatment; secreted protein; gene therapy; protein therapy; diagnosis; treatment; central nervous system; CNS; immune system; cancer; trauma; liver; reproductive disorder; congenital malformation; degenerative disease; inflammatory disease; neoplasia; metabolic disorder; testis; placenta; brain; T cell; spleen; lung; heart; rhabdomyosarcoma; endocrine system; endocrine polyglandular syndrome; endocrinema; espsis; endocrine ophthalmopathy; osteoclastoma; bacterial infection; bone; ds.
                                                                                                                                                                                              arathcargtnaaraartayaartgyggnytnathaarccntgyccngcnaaytayttyg 196
                                                                                                                                                                                                                                                                            cnttyaarathtgywsnggngcngcnaaygtngtnggnccnacnatgtgyttygargaym 256
Gaps
                                                                           ayatgwsnttywsnatgaaracnathmgnytnccnmgntggytngcnwsnccnacnaarg 136
                                                                                                                                                     414 NNNNNNTATTAGTATTAGGGTTATGGTATTTTATATTGCTAGCAAGACTTCCACCAATT 473
                                                                                                                                                                                                                                                                                                                 534 AATAATAACATIGTAAATGAGCTGTTGACACAGTGCAATAGTAAATAAAAATCGATAATA 593
                                    tnytnmgnytnytngcnytnathttygcnathgtnacnacntggatgttyathmgnwsnt 76
                                                                                                                                                                                                                       |: : |: || || || || || || || || AATCCAAGCCCAACAAAAAACTGTTGTTGTATATAAAATTTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human genes and secreted polypeptide(s) they encode useful for the diagnosis and treatment of e.g. cancers, CNS disorders, immune system disorders, inflammatory disease and
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  Indels
Mismatches 161;
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                                                                                                                                                                                                                                                                                                                                                           gnatgathatgwsnccngtnaaraayaaygt 287
                                                                                                                                                                                                                                                                                                                                                                                               594 GCATTAATAGATAAACGGAGATAAATCATCT 624
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WPI; 98-594496/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
  32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V69614/c
ID V69614 standard; DNA; 1341 BP
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530. .604
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/*tag= a
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605...742
    Conservative
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08-APR-1997; US-042728.
08-APR-1997; US-042754.
08-APR-1997; US-042825.
30-MAY-1997; US-048068.
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/*tag=
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US-042726.
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  78;
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useful for preventing, treating or ameliorating medical conditions e.g.

by protein of gene therapy. Also pathological conditions can be diagnosed
by determining the amount of the new polypeptides in a sample or by
determining the presence of mutations in the polynucleotides. Specific
uses are based on which tissues they are most highly expressed in, and
include developing products for the diagnosis or treatment of central
nervous system (CNS) and immune system diseases, reproductive disorders,
cancers, congenital malformations, degenerative diseases, traums,
inflammatory disease, neoplasia, metabolic disorders, diseases in testes,
inflammatory disease, rhabdomyosarcoma and disorders of the endocrine
system or other endocrinopathies, e.g. endocrine polyglandular syndrome,
endocrinoma, and endocrine ophthalmopathy, osteoclastoma and other bone
cendocrinoma, and endocrine ophthalmopathy, osteoclastoma and other bone
cendocling disorders, bacterial infections and sepsis. The polypeptides
are also useful for identifying their binding partners.
Sequence 1341 BP; 376 A; 278 C; 313 G; 373 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production processes
Example 8; Page 47-49; 77pp; English.
A xynB gene partial sequence (T08144) codes for a thermostable F-type xylanase (R87014) useful in the pulp and paper industries. The xynB gene, which codes for a multi-domain enzyme that includes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        521 tymgngaywsntgggtnttyathggngcnaargayytnmgnggnaarwsnccnttygarc 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 yaaygtnggnmgnggnytnaayathgcnytngtnaayggnacnacnggngcngtnytngg 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 553 CAACGTAGGAAGAGACAGAAACATTCTTCTTCTTCCACTTATTACCTGCCACTGTGTT--- 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               496 TTAAAAGGTATATGGTATTAAGAAAAGTTGGCTGTTGCGTTTTTTTAATTTTTAAATT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402 rathconggnggngcnytngtnytngtngcnwsntaygaygayconggnacnaaratgaa 461

    obtained

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          462 ygaygarwsnmgnaarytntt-ywsngayytnggnwsnwsntaygcnaarcarytnggnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               376 TGTGGTATCATATTAGGGATCCCATCAATGATTGGATAAGCTATTCCCAACTCTTCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 ncaraargcnttygayatgtaywsnggngaygtnatgcayytngtnaarttyytnaarga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xylanase xynB gene (partial sequence).
Xylanase B; xynB gene; thermostable enzyme; paper; pulp; lignin; delignification; xylan; bleaching; ds.
Extremophile isolate TG456 (CBS 213.94).
21-DEC-1995.
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from anaerobic thermophilic bacteria and used in paper and pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gronberg
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.5%; Score 37; DB 1; Length 1341; Best Local Similarity 28.3%; Pred. No. 0.77; Matches 91; Conservative 60; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S, Gronber
Morgan HW;
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14-JUN-1994; EP-201699.
(KONN ) GIST-BROCADES BV.
Bergquist PL. Daniel RM,
Herweiler MA, IVerson S, JO
Ouax WJ. Williams DP;
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P-PSDB; R87014.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This DNA encodes a human interleukin-12 (IL-12) p40 subunit. This is used in the construction of plasmid for expressing recombinant eukaryotic genes. The plasmid comprises a first transcription unit comprising control sequences linked, in order, to a 5'-untranslated region (UTR),
single xylanase B domain, was obtd. by genomic walking PCR of DNA from extreme thermophilic strain TG456 (CBS 213.94), isolated from a New Zealand hot spring. The gene can be inserted into a vector and used for the prodn. of recombinant xylanase B in microbial host cells, esp. Escherichia coli.

Sequence 1633 BP; 564 A; 291 C; 347 G; 431 T;
                                                                                                                                                                                                                                                                                                                          409 GCACAGAGCAATAATATGGAATAAGAGGTCATACACTGGTTTGGCATCAACAAACTCCA 468
                                                                                                                                                                                                                                                                                                                                                                       509 arcarytnggnttymgngaywsntgggtnttyathggngcnaargayytnmgnggnaarw 568
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmids for co-ordinated expression of recombinant eukaryotic genes-useful for, e.g. therapeutic gene delivery, especially for treating asthma and cancer Disclosure; Fig 4A-D; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "human IL-12 p40 subunit"
/note= "the protein is encoded by degenerate codons
which can code for each of the amino acid"
                                                                                                                                                                                                                                                                               449 gnacnaaratgaaygaygarwsnmgnaarytnttywsngayytnggnwsnwsntaygcna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469 GATTGGTTTTTCCAGCATTCTGACGGTTCGCCACTTGATCCAAACAATTCTGAAGACAAG
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Human interleukin-12 (IL-12) p40 subunit encoding DNA.
Interleukin-12; IL-12; p40 subunit; p35 subunit; human; asthma; cancer; therapeutic gene delivery; vaccine; allergy; ss.
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                                                                                                                                                                                    Length 1633;
                                                                                                                                                                                                                               41; Mismatches 106; Indels
                                                                                                                                                                                    5.5%; Score 36.8; 27.9%; Pred. No. 1;
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WPI; 98-261507/23.
P-PSDB; W57482.
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                                                                                                                                                                                       Query Match 5.5%
Best Local Similarity 27.9%
Matches 57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-1997; U18832.
18-OCT-1996; US-028687.
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                                  Query Match 5.5%; Score 36.6; DB 1; Best Local Similarity 10.0%; Pred. No. 0.79; Matches 60; Conservative 154; Mismatches 387;
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A composite CDNA sequence (T30309) codes for the human transcription factor, SOX-9 (R97646). It was deduced from cDNA clones obtd. from a testis CDNA inhibrary using a SOXA HMG (high mobility gp.) probe. The gene appears to play a role in skeletal development. It has been mapped to chromosome 17 within a region which contains CMPD!, the locus for camponelic dysplasia (CD). Alterations in SOX-9 can cause both CD and male to female sex reversal. The cDNA can be used in the prepn. of recombinant SOX-9 polypeptide. DNA or recombinant protein may be injected into joint tissue for treatment of cartilage or bone damage. SOX-9 can also be used as a tool for studying bone formation and sex determination. Sequence 3934 BP; 966 A; 1100 C; 901 G; 967 T;
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                                                                                                                                                            or suppression of bone or cartilage differentiation or growth
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Koopman PA;
                                                                                                               New isolated SOX-9 genes
Goodfellow PN, Koo
WPI; 96-27777/28.
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Search completed: May 31, 2000, 19:04:01 Job time: 5944 sec

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1 (bases 1 to 1606)
Bione, S., Tamanini, F., Maestrini, E., Tribioli, C., Poustka, A., Torri, G., Rivella, S., and Toniolo, D.
Transcriptional organization of a 450-kb region of the human obroonsome in Xq28
Proc. Natl. Acad. Sci. U.S.A. 90 (23), 10977-10981 (1993)
                                    01-DEC-1998
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361 CCAGAGCTGCAGGATGGAGGCTGCATGCCCCCGAAGCCATTT 405
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44.0%; Score 294.6; DB 5;
Best Local Similarity 59.3%; Pred. No. 1.4e-61;
Matches 240; Conservative 93; Mismatches 72;
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Yu,G. and Rosen,C.
Colon specific genes and proteins
Patent: US 5733748-A 6 31 MAR-1998;
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/translation="MRLAGPLRIVVLVVSVGVTWIVVSILLGGPGSGFPRIOQLFTSP
BSYVTAAPRAKKYGGLPQPCPEEHHAFRVVSSAANVIGPKTGLEDKHAMSSYKDNVG
RGINIALVNGVSGELIEARAPROMAGDVNDLLKFIRPLHEGTLVFVASYDDPATKMNE
BTRKLFSELGSRNAKELAFRDSWVFVGAKGVONKSPFEQHVKNSKHSNKYEGCPBALE
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                                                            Instituto di Genetica
Via Abbiategrasso 207, 27100
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                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA60645.1"
/db_xref="GI:854082"
/db_xref="SWISS-PROT:P98173"
                                  Direct Submission
Submitted (09-MAY-1995) D. Toniolo,
Biochimica ed Evoluzionistica, CNR,
                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="x"
/cell_line="fetal brain"
/clone_lib="lambda ZAP"
/map="q28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281
                                                                                                                      Location/Qualifiers
1. .1606
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                                                                                                                                                                                                                                                                                                       /gene="2.19"
278. 970
/gene="2.19"
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1588. .1593
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521 c
(bases 1 to 1606)
                                                                                                       Pavia, ITALY
                   Toniolo, D.
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BASE COUNT 301
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809

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451 acnaaratgaaygaygarwsnmgnaarytnttywsngayytnggnwsnwsntaygcnaar 510
                                                                                                                                    511 carytnggnttymgngaywsntgggtnttyathggngcnaargayytnmgnggnaarwsn
                               631 ytnytngaratggarggntgyatgccnccnaarc 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="EF-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 465) Fu, X. and Kamps, M.P.
                                                                                                                                                                                                                                                                                                                                                      U72677.1 GI:1872484
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/protein_id="BAA13251.1"
/protein_id="BAA13251.1"
/db_xref="01:1507674"
/tbanslation="mrvagaakLvvavavelltffYvIsQvFEIKMDASLGNIFARSAL
DTAARSTRAPRRYKGISKACPEKHFRFKMASGAANVVGPKICLEDNYLMSGVKNNVGR
GINVALANGKTGEVLDTKYFDMWGGDVAPFIEFLKAIQDGTIVLMGTYDDGATKLNDE
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                                                                                                                                                                                                                                                                                                                                                                    The cloning of a cDNA for novel genes expressed in human osteoblast Unpublished (1996)
                                                                                                                                                                                                                             Direct Submission
Submitted (14-AUG-1996) to the DDBJ/EMBL/GenBank databases. Ikko
Ohno, Institute for Molecular and Cellular Biology, Osaka
University, Molecular Genetics; 1-3 Yamada-Oka, Suita, Osaka
Japan (E-mail:kousaku@imcb.osaka-u.ac.jp, Tel:81-6-879-7992,
Z (Bases 1 to 2475)
Ohno,I., Hashimoto,J., Takaoka,K., Ochi,T., Okubo,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 AGTGGAGCAGCCAACGTGGTGGGACCCCAAAATCTGCCTGGAAGATAATGTTTAATGAGT 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 gcngtnytnggncaraargcnttygayatgtaywsnggngaygtnatgcayytngtnaar 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens cancellous bone tissue_lib:3 end-directed library osteoblast cell_line:primary-cultured cDNA to mRNA, clone_lib:lambda ZAP clone:GS3786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 AGATATAAGTGTGGGATCTCAAAAGCTTGCCCTGAGAAGCATTTTGCTTTTAAAATGGCA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                              11-MAR-1998
                                                                                                                                                             Bukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Butheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2475)
Ohno,I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aartayaartgyggnytnathaarccntgyccngcnaaytayttygcnttyaarathtgy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 510 GAAGTATTAGACACTAAATATTTTGACATGTGGGGAGGAGATGTGGCCACCATTTATTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 248.2; DB 9; Length
; Pred. No. 4.2e-50;
94; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers

1. 2475
Acranism="Homo sapiens"

(db.xref="taxon:9606"

/cell_line="primary-cultured"

/cell_type="osteoblast"

/clone=ib="lambda ZAP"

/tissue_lib="lambda ZAP"

/tissue_lib="a and-directed library"

/tissue_type="cancellous bone"

168.851
                               PRI
cds.
                 DB7120 2475 bp mRNA
Homo sapiens mRNA for GS3786, complete
D87120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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47.98;
                                                                         D87120.1 GI:1507673
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1 380 c
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                                                                                                                                                       Homo sapiens
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Best Local Similarity
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                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 CTGAACTTCCTTACGGAAATTCCAGATAGCACCCTGGTGCTGGTGGTAGCTCCTTATGATGATGA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acnggngcngtnytnggncaraargcnttygayatgtaywsnggngaygtnatgcayytn 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (27-SEP-1996) Pathology, University of Callfornia,
Diego, 9500 Gilman Drive, La Jolla, CA 92093, USA
              29-MAR-1997
                                                                                                                                                           Mammalia;
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 465)
Fu,X. and Kamps,M.P.
E2a-Pbx1 induces aberrant expression of tissue-specific and developmentally regulated genes when expressed in NIH 3T3 fibroblasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="BALB/c"
/db_xref="taxon:10090"
/coll_line="NIH373"
/cell_type="E2a-Pbx1 induced fibroblasts"
complement(117. .>465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein"
              ROD
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                                                                                                                                                                                                                                                                                      Mol. Cell. Biol. 17 (3), 1503-1512 (1997)
97184476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.4%; Score 189.8; DB 1
49.9%; Pred. No. 5.4e-36;
ive 74; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to human 2.19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ده
MMU72677 465 bp mRNA
Mus musculus EF-7 mRNA, partial cds.
U72677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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MO 63108, USA
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Waterston, R.H. The sequence of Homo sapiens clone Unpublished
                                                                                                                     ccnggnacnaaratgaaygaygarwsnmgnaarytnttywsngayytnggnwsnwsntay
                                                                                               genaarcarytnggnttymgngaywsntgggtnttyathggngenaargayytnmgnggn
                                                                                                                                                                                           aarwsnccnttygarcarttyytnaaraaywsnccngayacnaayaartaygarggntgg
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* NOTE: This is a 'working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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HTG; HTGS_PHASE1.
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Waterston, R.H.
Direct Submission
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KEYWORDS
SOURCE
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COMMENT

us-09-186-342-8.rge

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join(3351. .3470,13327. .13364,13460. .13568,14110. .14335,
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16701. .16936,17041. .17117,17223. .17315,17413. .17503)
/gene="GGPD"
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                                    1-20114 bp: 6 corrections made from X55448, including 8850 (delete T), 14575 (add C), 18788 (delete C), 19369 (delete G), 19389 (delete G), and 19480 (T changes to A); G6PD: Glucose-6-phosphate Dehydrogenase
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/translation="MAEQVALSRTQVCGILREELFQGDAFHQSDTHIFIIMGASGDLA
KKKIYPTIWWLFRDGLLPENTFIMGYARSRLTVADIRKQSEPFFKATPEEKLKLEDFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARNSYVAGQYDDAASYQRLNSHMDALHLGSQANRLFYLALPPTVYEAVTKNIHESCMS
QIGWNRIIVEKPFGRDLQSSDRLSNHISSLFREDQIYRIDHYLGKEMVQNLMVLRFAN
               /note="1-20111 bp replaces previous submission X55448,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="glucose-6-phosphate dehydrogenase"
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2252. .18112
/gene="GGPD"
3343. .3470
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/gene="G6PD"
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16375. .16561
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/gene="G6PD"
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15007. .15
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1 (bases 1 to 52173)
2010, M., Mazzarella, R., Bione, S., Toniolo, D., Schlessinger, D., D'Urso, M. and Chen, E.Y.
Sequence and gene content of the RCP/GCP-G6PD region in human Xq28: the first 52kb
Unpublished
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Submitted (12-JaN-1994) Ellson Y Chen Dr., Advanced Center for Genetic Technology, Applied, Blosystems Division, Perkin Elmer Corp., 850 Lincoln Centre Drive, Foster City, CA, 94404, USA On Jan 26, 1994 this sequence version replaced gi:31540.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen, E.Y., Cheng, A., Lee, A., Kuang, W.J., Hillier, L., Green, P., Schlessinger, D., Ciccodicola, A. and D'Urso, M. Sequence of human glucose-6-phosphate dehydrogenase cloned in plasmids and a yeast artificial chromosome Genomics 10 (3), 792-800 (1991)
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H.sapiens G6PD gene for glucose-6-phosphate dehydrogenase.
X55448 25927
X55481 G1:450527
2-19 protein; G6PD gene; glucose-6-phosphate dehydrogenase.
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8553 147398: contig of 8846 bp in length
7399 147416: gap of unknown length
7417 155917: contig of 8501 bp in length
5918 155935: gap of unknown length
8243 168242: contig of 12307 bp in length
8343 168259: gap of unknown length
8360 178137: contig of 9878 bp in length.
Location/Qualifiers
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ilarity 52.7%; Pred. No. 2.9e-11;
Conservative 39; Mismatches 23;
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                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/db_xxef="taxon:9606"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                     /clone="RP11-475023"
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Chen, E.Y.
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Matches 69; Conserv
                                          147399
147417
155918
155936
168243
168260
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HSG6PDGEN
LOCUS
                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
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144140.1 GI:1203968

144140.1 GI:1203968

14 gene; 2_19 gene; ABP-280 gene; DNL1L gene; DNase I-11ke protein

14 gene; EMD gene; FLN gene; G4.8 gene; G6PD gene; GDI

15 gene; GdX gene; P3 gene; GM gene; STA gene; XAP-1 gene; XAP-2 gene;

15 gene; XAP-5 gene; XAP-7 gene; actin-binding protein; emerin;

16 gene; ABP-5 gene; Talamin; glucose-6-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Long-range sequence analysis in Xq28: thirteen known and six candidate genes in 219.4 kb of high GC DNA between the RCP/GCP and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 21947)
Chen,E.Y., Zollo,M., Mazzarella,R.A., Ciccodicola,A., Chen,C.-N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine,
St. Louis MO 63110 USA
e-mail: ellson@genseq.apldbio.com and davids@genetics.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Molecular Microbiology and Center for Genetics in
                                                                                                                                                                                                                                                                                                                                                                                       Ellson Chen,
Advanced Center for Genetic Technology,
Applied Blosystems Division of Perlin Elmer Corp., 850 Lincoln
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's.
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                                                                                                                                                                                                                                                                                                                 Length 52173;
                                                                                                                                                                                                                                                                                                                                                     40; Indels
                                                                                                                                                                                                                                                                                                               ch 11.4%; Score 76.2; DB 9; 1.1 Similarity 45.4%; Pred. No. 8.1e-08; 64; Conservative 37; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hum. Mol. Genet. 5 (5), 659-668 (1996)
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41815 CAAGAGCCCCTTTGAGCAGGT 41835
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                                         /number=4
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Best Local S
Matches 64
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HUMFLNG6PD/c
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40689. .40747,41175. .41225,41546. .41630,41707. .41833,
42131. .42226)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-"MRLAGPLRIVVLVVSVGVTWIVVSILLGGGGSGFPRIQQLFTSP
BSSYVAAPRAKKGGLPQPCPEEHHAFRVVSGANVIGPKTGLEDKMLMSSYKDNVG
RGIAITALVNGVSGELIERARAPUMMAGDVNDLLKFIRPLHEGTLVFVASYDDFATKNNE
ETRKLFSELGSRNAKELAFRDSWVFVGAKGVQNKSPFEQHVRNSKHSNKYEGCPEALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="downstream G6PD intergenic region"
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                                                                                       /note="near the end of intron 11"
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33000. 42862
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18112
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                                                                    /gene="G6PD"
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                                    'number=11
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/number=48
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                                1.1 and 1.2, coupled with fasta and blastx comparisons to genbank
                                                                  non-redundant peptide libraries. Repeat analysis was accomplished
Note: Gene predictions were accomplished with runs of Grail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(7358. 7432)
/rpt_family="Alu-Sb0 or Alu-Sb1"
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complement(3663. .3952)
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/evidence=experimental
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/vpt_family="Alu-Sx"
/evidence=experimental
complement(8863. 9029)
/rpt_family="Alu-J or Alu-S"
/evidence=experimental
complement(9031. 9317)
/rpt_family="Alu-Sq"
/evidence=experimental
complement(9318. 9942)
/rpt_family="Alu-J or Alu-S"
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/rpt_family="Alu-Sx"
/rpt_denent(1446. 1536)
/rpt_family="Alu-J"
                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
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complement(7121. .7409)
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/evidence=experimental
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QLENVSVALEFILDRESIKLVSIDSKAIVDGNLKLILGLIWTLILHYSISMPMWDEEED
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ö Gaps 11.4%; Score 76.2; DB 40; Length 219447; 45.4%; Pred. No. 1.1e-07; 37; Mismatches 40; Indels Query Match Best Local Similarity 45.4%; Matches 64; Conservative

444 yccnggnacnaaratgaaygaygarwsnmgnaarytnttywsngayytnggnwsnwsnta 503 à

504 ygcnaarcarytnggnttymgngaywsntgggtnttyathggngcnaargayytnmgngg 563 à

ACO06364 132319 bp DNA PRI 21-DEC-199 Homo sapiens BAC clone GS1-146J4 from 7q31.1-31.3, complete sequence. ACÓ06364 ACO06364.3 GI:4753253 Homo sapiens human. DEFINITION ORGANISM AUTHORS TITLE ACCESSION REFERENCE VERSION KEYWORDS SOURCE AC006364

2 (bases 1 to 132319)
Ryan,E., Bauer,C., Tucci,S. and Spalding,L.
The sequence of Homo sapiens BAC clone GS1-146J4
Unpublished JOURNAL REFERENCE AUTHORS TITLE

Waterston, R.H. TITLE AUTHORS

MO 63108, USA 4 (bases 1 to 132319) Waterston, R.H. MO 63108, USA AUTHORS JOURNAL REFERENCE

(bases 1 to 132319) Direct Submission TITLE AUTHORS REFERENCE

RESULT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 132319)
Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998) JOURNAL MEDLINE REFERENCE

Direct Submission Submitted (11-JAN-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, (bases 1 to 132319)

Direct Submission Submitted (05-MAY-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.

Submitted (11-SEP-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington
Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On May 5, 1999 this sequence version replaced gi:4337266. 6 (bases 1 to 132319) Waterston, R. TITLE JOURNAL AUTHORS REFERENCE COMMENT

Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu Center code: WUGSC

Center project name: H_GS146J04

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions. all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted:

restriction diqest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov, or see http://genome.wustl.edu/gsc

This clone is from the first BAC library from Genome Systems, Inc (http://www.genomesystems.com). Cell line: lymphoblastoid SOURCE INFORMATION:

pBeloBAC Haplotypes:

The actual start of this clone is at base position 1 of GS1-146J4; actual end is at 132319 of GS1-146J4. Selection: chloramphenicol NEIGHBORING SEQUENCE INFORMATION:

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                                                                                                                                                                                                                                                                                                                   Length 132319;
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11 Similarity 34.2%; Pred. No. 0.00041;
64; Conservative 43; Mismatches 86
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Miller,N., Wamsley,P. and Twyman,B.
The sequence of C. elegans cosmid M70
Unpublished (1998)
3 (bases 1 to 37777)
Waterston,R.
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94150718
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TITLE
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11766. 12114

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                                                                                                                                                                                                                                          misc_feature
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                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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COMMENT

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RASTATARKSELATIK SVERAILDATMOGLDTLSKLAPPHSAVKVESFYENSAFROITI
RASTATARKSELATIK SVERAILDATMOGLDTLSKLAPPHSAVKVESFYENSAFROITI
SKTSDVNSWDADIRNIKKLPVTIRKMSTVASRSTNIFGKYTAGFSNGVODLOKIEV
DLKDEWIOKTWRTVDGLKRFEGTTAAVLDGKLKGVQTMKHSASEAARLEKLIENS
RNDOISAKKVIDSTILCKTFSVGSHVKSVTASQUOGLLETTANAKKISELIATISKL
GNSLDSIPVETLKTFTRQLKSSVALIKNRFTVALLATKLKSESDLIVEFKENGIVKPV
IGYPOLKNKKNDFGPGISNVLEVALKLREKSDQOFFKNLETKASGRAGSSSIRVPN
DALSNIKKNKNTGEVGMLKDLOKYSLPLGSVATAITWSGKVLEKKAALYSIEDGDTV
EGGLISVSSBALNLAVGSKYODFHALCHSLVLLLGKLESWRSSIKKPANDTLVALTAM
FKGLSQLPSVDIQADIKILAIDELSGKLKDDSQOKLDELKSSLQSVBPLDLQFSFNV
GPLNDISTTLNGLALVFSNANKTLSGKTAGNGOSSNSMITITEVSILIPLILII
VVLILMSRKLLCFKKKDTFFREARVPROVPNPTPQTAKVPPARPPRADEKPKDVNV
KKAETEKPKTEVTPRAANKSASKVDATNTTTEDGSTONNTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(10513. ,10570,10619. ,10678,10755. ,10814,11327. ,11386,
11444. ,13526,13578. ,13932,15821. ,15970)
/gene="M70.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MTITTLFTWLICFFLWYASRRFEKKKIHYPSRRORFVDYLINA
QRSEKLELHSQQQFGNRHLGCDELVKSENREKAKSTKKKEKVKSEKMKKATATTGAGS
TIDQSSKDPTRTTMASERGMTWTQRVQKEKSIKKTNSELKAAADNQTVTQGNDTTTTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAC04435.1"
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/dc_xref="G1:29118688"
/dc_xref="G1:2911888"
/dc_xref="G1:2911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QANFIKHLSKDRAHLKMKKLSKMPPVDSAKFDLTYPLGYTFDTKSDSWYTNOPYFCE
GDGFKGESKIYKIYAGCDKKIAKFEDIKDSKIQNPSAITVYKEGSQIAVLCSDNSKRP
SIRLIDLKNSSHKASTFCSYKDRKIDFSHPARGLARTIGGNLITMDRPPPEEGDPRLR
KVLEKKDDLYSIVEDGKTVEEGLSSPNERLKRAVSSKWGDFSALQHNLVLLGKLESW
KSSIKKPANDTLVALTAMFKGLSQLPSVDIQADLKISAIDDLLPLPISGKPKLDELKS
SLQSVEPLDLQFSKFNGALKDISTTFNGLQLVFSSGKTGNKTVSKGPAAVKKAQASTP
                                                                                                                                         PPASDNSMAIIIAVSVAVVLVASILIVAGLWFFGFLPFCPRKKNSKTAGRDQKGKSKK
TKKGKSKSGKEPVPISEATNSTPSGEDGSKIDTISKSKTEPIRAPFKDEGNYEDLAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="IQLHLSRQTALTEEDILNVKNLNFFSPRPQESTETLPGTSNSRI
DEPEELEELDYNESLSDWSESQRSAEELAEEDELNFVENGLNDVKIESEIEETAYFPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPPETAENAWEILKNLQILKEKAIKTEEEEDIIYLSSDSESEDAEAERDDFLQKSNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VFRVDDDRRKTAVSDETFVLSGTSLPSFIATSGDTVVITDLGKQQTVILIRLDDSKWK
VRKEIIRVSTOSAGINLSABHILNTQYFTYVAGAQIDQNGNVIIADAKNHFKLFEPS
LGFIHRVSTDFPVPVSSFHVNHRGECLILSIRDTQKVHFARLSSTNRLEPHIKSGAG
KRQCYTNPLSSKRLAISD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .31640,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(29295. .29447,30527. .30619,31518. 33056. .33487,35402. .35661,37257. .>37776))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="coded for by C. elegans cDNA yk50e3.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 34; Length 37777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.8%; Score 52; DB 34; Length 37 33.8%; Pred. No. 0.061; Live 35; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPSSLFPADLSKKDRLRLGKVKERAVAAPEKKKTKNKE"
10513. 15970
/gene="M70.1"
                                                                                                                                                                                                                                                                                                                                                                               join(7676. .7746,7790. .8315)
/gene="M70.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEGAVPIDWPKDVKPPPRNLKLNINEI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              u
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/protein_id="AAC04438.1"
/db_xref="GI:2911871"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/protein_id="AAC04436.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(29295. .>37776)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6462 g 12594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                        /gene="M70.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="M70.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="M70.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6561 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12160 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                     gene
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                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Jobe = "coded for by C. elegans cDNA yk150h9.5; coded for hy C. elegans cDNA yk199.5; coded for by C. elegans cDNA yk268.3; coded for by C. elegans cDNA yk268.3; coded for by C. elegans cDNA yk268.3; coded for by C. elegans cDNA yk101e8.3; coded for by C. elegans cDNA yk101e8.3; coded for by C. elegans cDNA yk101e8.3; coded for by C. elegans cDNA yk239e5.3; coded for by C. elegans cDNA yk239e5.3; coded for by C. elegans cDNA yk239e5.5; coded for by C. elegans cDNA yk260c1.3; coded for by C. elegans cDNA yk260c1.5; coded for by C. elegans cDNA yk260c1.5; coded for by C. elegans cDNA yk316h12.5; coded for by C. elegans cDNA yk317f7.5; coded for by C. elegans cDNA yk317f7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAKWEEASEKISGAGSVDLHKAIVDAQTVRTWWRNVGDLNSIPDKEAFKVFEKIEKLD
LKIFEIFANSETLKLLDSRASIATAKKSLEAIIKSYRSAIDATNGGLDTLSKLAPFHS
AVRVESFYENASKDIISKPSDGKSMDDIENIKKLPVTTIFKLMSYVASRSTNILG
KYRVESFSENAVQDLQKIEVDLKDEWIQKTMNRTVDGIKKGVGT
MKHSASESANAVQDLQKIEVDLKDEWIQKTMNRTVDGIKKGVGT
MKHSASESANALEKLIQMSSNAPISAQTIGSIKPCTPVAVDGKKGVGVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKKNILIIIGILLISVFCISSGSAPFKQSETAKTSDFTAFSNAH
NIIIASGSSPSKQSETAKTSHFTDFSNAHNVIRDSPPQFKPNKFLHRVKRAENDYAYS
LLMKRIPMLARVVSAISLYNGLVDNSIPSDEAITDLLNIGGVKLKDLETFDKTKVDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERTLMAVKKISELIATSKLGNSLDSIPVETLKTFTRQLKSSVALTKNRETVALLATKL
KSESDLIVEFKENGIVKPVIGVFDCLKNKKDDFGPISNVLEVALKLRELKSNQEFFTN
LEEISSEIAGSSSPIKSIRDAIANIKKSNNTEDLILLKDLQKYSAPLGNVATALVNAE
                                                Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The 5' cosmid is T04C4, 200 bp overlap; 3' cosmid is C37F5, 250 bp overlap. Actual start of this cosmid is at base position 197 of CELM70; actual end is at 37777 of CELM70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TICE: This sequence may not be the entire insert of this clor may be shorter because we only sequence overlapping sections se, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         finished as follows unless otherwise noted:
                                                                                                                                                                                     Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, NO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(2333. .2407,2799. .3093,3145. .52.
5288. .5347,5954. .6040,6795. .6881,6952. .7009))
/gene="M70.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIGHBORING COSMID INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Caenorhabditis elegans"
/strain="Bristol N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAC04437.1"
/db_xref="GI:2911870"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(2333. .7009)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:6239"
/chromosome="IV"
              Direct Submission
Submitted (11-FEB-1998)
University, 4444 Forest
Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neighboring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="M70.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="M70"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sedneuce was
              TITLE
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Db 102586 CTIGGAAGAAIGGCTIGACGCGGIGCCGACCGGCTACATIGIAGCCGTIGIGAGCTITCGA 102527
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                                                                                                                                                                                                                                                                                                           Length 151727;
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105 114914: gap of unknown length
315 118859: contig of 3945 bp in length
860 118869: gap of unknown length
516 12652: gap of unknown length
526 128766: contig of 2241 bp in length
527 128776: gap of unknown length
777 145383: contig of 16607 bp in length
1384 145392: gap of unknown length
15727: contig of 6335 bp in length
15727: contig of 6335 bp in length
160cation/Qualifiers
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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
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                                                                                                                                                                                             7.3%; Score 48.6; DB 5; I
ilarity 9.9%; Pred. No. 0.29;
Conservative 169; Mismatches 214;
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33.8%; Pred. No. 0.083;
tive 35; Mismatches 98
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Best Local Similarity 33.8%
Matches 68; Conservative
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Best Local Similarity
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Submitted (24-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

On Mar 1, 1999 this sequence version replaced gi:4263454.

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 19 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 151727)
Waterston, R.H.
The sequence of Caehorhabditis elegans clone
                                                            23190 CGAGGCCTCTAATCAGCTGTCAGATATGGCTCGGCGCGATCTTTTACGAGATGGGCTCCAG 23131
23250 CTIGGAAGAATGGCTTGACGCGGTGCCGACCGGCTACATTGTAGCCGTTGTGAGCTTCGA 23191
                                                                                                               AC006894 151727 bp DNA HTG 26-FEB-1999 Caenorhabditis elegans clone Y71G10, *** SEQUENCING IN PROGRESS
                               441 ygayccnggnacnaaratgaaygaygarwsnmgnaarytnttywsngayytnggnwsnws 500
                                                                                            501 ntaygcnaarcarytnggnttymgngaywsntgggtnttyathggngcnaargayytnmg
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contig of 2961 bp in length
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of 9128 bp in length
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Waterston, R.H.
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Yeary, Z. Jahag, C., Luo, L., Ouyang, S., Zhang, S., Li, W., Wu, J.,
Zhou, S., Liu, M., and He, F.
Direct Submission
Direct Submission
Direct Rediation Medcine, 27 Talping RD, Beijing 100850,
P.R.China
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taywsnggngaygtnatgcayytngtnaarttyytnaargarathccnggnggngcnytn 420
                                                          gtnytngtngcnwsntaygaygayccnggnacnaaratgaaygaygarwsnmgnaarytn 480
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1 (bases 1 to 1302)

Yu,Y., Zhang,C., Luo,L., Ouyang,S., Zhang,S., Li,W., Wu,J., Zhou,S., Liu,M. and He,F.

Functional prediction of the coding sequences of 50 new genes deduced by analysis of cDNA clones from human fetal liver Unpublished
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llarity 14.0%; Pred. No. 0.25;
Conservative 97; Mismatches 105;
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    1302
    /organism="Homo sapiens"
/db_xref="taxon:9606"

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/dev_stage="fetus"
217 c 179 q
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VVIAGEPWYGKSSLLNLLSGQETAIYDIAGTTRDIIRESHIDGLEHVUOTAGLRL
TEDVVEKEGVRRTQKAVQADLLLLINIDASKPTEDFKKIIAQWFSENDNKIPTLIVEN
KIDLIGEARKENVEYPHIKLSVYRTRAGVELLKNHLKNTAGFEATHENNFIARRRHCD
AIARASAFLKNANNHLLNQKAGELVAEDLKLAQNALSEITGEFTSDDLLGKIFSEFCI
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PRYATFVKFRDSGSVIDEGIALYFPKPNSFTGEDVLELHGHGGPVVMDRLLNTVLKAG
ARQARPGEFSERAFLNNKIDLAQAEAVADLINASSEQAARSAMKSLQGEFSKRIHQLV
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Omscnpaiggigkshlvkeidalggimalaadoagihfrtlnarkgpavratraoadr
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1 (bases 1 to 6031)
Willems, H., Jager, C. and Baljer, G.
Physical and genetic map of the obligate intracellular bacterium Coxiella burnetii
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Submitted (08-JAN-1997) H. Willems, Institute fuer Hyggiene und,
Infektionskrankheiten der, Tiere Justus-Liebig-Universitaet,
Frankfurterstr 89, 35392 Giessen, FRG
Location/Qualifiers
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/note="orf452; translated orf similarity to SWISS-PROT:
THDE_PSEPU thiophene and furan oxidation protein of
Pseudomonas putida"
/codon_start=1
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662 TYCYKRWKGKYCMWKSMMYTYMWYYKGGSCYKSMRKKRAAAARKWWTYYWKTKGR 721
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/note="orf627; translated orf similarity to SWISS-PRG GIDA_ECOL1 and GIDA_PSEPU glucose inhibited division protein A of E.coli and Pseudomonas putida"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA BCT 19-JAN-1999 for encoding glucose inhibited division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y10436.1 GI:1780758
glucose inhibited division protein; glycyl-tRNA synthetase. Coxiella burnetii.
coxiella burnetii
                                                                                                                                                494 gnwsnwsntaygcnaarcarytnggnttymgngaywsntgggtnttyathggngc 548
                                                                                                                                                                                                                   Bacteriol. 180 (15), 3816-3822 (1998)
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/db_xref="GI:1780760"
/db_xref="SWISS-PROT:P94613"
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/db_xref="G1:1780759"
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protein A and B.
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On Feb 16, 2000 this sequence version replaced gi:6691734.
INDRYANY: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding
                                                                                                            The sequence may
                                                                                                   that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. order of seqments is not known; 800 n's separate segments. Contig_ID: 00092 Length: 2632bp
                                                                                                                                                                                                                                                                                                    Contig_ID: 00352 Length: 38824bp
Contig_ID: 00590 Length: 3802bp
Contig_ID: 00595 Length: 2557bp
Contig_ID: 00954 Length: 2557bp
Contig_ID: 00995 Length: 2585bp
Contig_ID: 00995 Length: 4156bp
Contig_ID: 01393 Length: 4115bp
Contig_ID: 01637 Length: 4115bp
Contig_ID: 01637 Length: 11549bp
Contig_ID: 01637 Length: 13589bp
Contig_ID: 01637 Length: 13502bp
Contig_ID: 01707 Length: 32002bp
Contig_ID: 02080 Length: 33002bp
Contig_ID: 02080 Length: 1378bp
Contig_ID: 02194 Length: 13745bp
Contig_ID: 02276 Length: 13745bp

Contig_ID: 02276 Length: 13745bp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pleces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 3432; gap of 200 bp 343 7164: contig of 3732 bp in length 7165 7964: gap of 800 bp 7165 7964: gap of 800 bp 7165 1250: contig of 9286 bp in length 1725 18050: gap of 800 bp 800 bp 18051 31751: contig of 13701 bp in length 31752 32551: gap of 800 bp 72155 32551: gap of 800 bp 72175 3600: contig of 38024 bp in length 71376 72175: gap of 800 bp 72176 76080: contig of 3805 bp in length 76080: gap of 800 bp
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149058: contig of 14267 bp in length
9888: gap of 800 bp
181860: contig of 32002 bp in length
2660: gap of 800 bp
185978: contig of 3318 bp in length
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109253 113553: contig of 4319 bp in length
13554 114353: gap of 800 bp
114354 125902: contig of 11549 bp in length
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108434: contig of 14516 bp in length
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79437: contig of 2557 bp in length
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96 bp in length
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86933: contig of 6696
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Length: 13701bp
Length: 38824bp
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Contig_ID: 00365
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   COMMENT
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IQPGRYQPRRQMDKDALEELANSIRAQGIIQPIVARPVGQRYEIIAGERRWRAAQLAG
ICROPANTPITDEAAITMSLIENIQRQNLNAIEBAALQRLLDEFKWTHEEIAARVG
KSRTSVTNSLRLIKKINPDVRALLEGGHLDMGHARALLALGFGQGSBANIIIKRALSV
RETEKLIQHWQSEGKSSANRPSMDPDVARLQHHLSDKLGAAVTIRHGAKGKCKLIHY
                                                                                                                                                                                           /transl_table=11
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/db_xref="S-PROT:P94614"
/translation="WTEKLKQGIDQLGLKVAETIQQSMLAFLAFLQKWNQAYNLFAIT
                                                                                                                                                                                                                                                                                                                                     EIKSMITHHLLDSLSILPYIKGDKILDVGSGAGFPGIPLAFACPEKKFTLIDSKAKKT
AFLLQAASRFKITNVTIIQERVGSYQPGFYFDTITCRALGSVREIMEGTNHLLRSGGQ
WLIMKGAYPEKELRGTDASAIVHVLNVPGLKAERHLVEVKNNKG"
   1TAQIPSSLDYNQVTGLSNEVRQKLNETKPTTLGQASRIPGITPAAISLLLVHLKKKE
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/note="orf2080; translated orf similarity to SWISS-PROT:
YG12_PSEPU hypothetical 32.4 kDa protein of Pseudomomas
                              3782. .4396
/note="orf256; translated orf similarity to SWISS-PROT:
YGI1_PSEPU hypothetical 28.9 kDa protein of Pseudomonas
putida"
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Submitted (15-JAN-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, Wr. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
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*** SEQUENCING IN
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 222877)
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28.8%; Pred. No. 0.39;
ive 47; Mismatches 114; Indels
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Homo sapiens chromosome 6 clone RP1-295F6, PROGRESS ***, 19 unordered pieces.
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/protein_id="CAA71461.1"
/db_xref="G1;1780762"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Matches 65; Conservative
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SOURCE
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Search completed: May 31, 2000, 18:42:56 Job time: 5915 sec
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Submitted (23-FEB-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Caenorhabditis elegans clone Y38F2, *** SEQUENCING IN PROGRESS ***, ACOO6745
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Waterston, R.H.
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                                                                                                                                                                                                Query Match 6.6%; Score 44; DB 32; Length 222877; Best Local Similarity 29.0%; Pred. No. 8.1; Matches 76; Conservative 44; Mismatches 142; Indels 0;
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                                                                                        /clone_lib="RPCI-1"
44516 c 43322 g 60358 t 14403 others
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/chromosome="6"
/clone="RP1-295F6"
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Waterston, R.H.
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    .249287
    /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"

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Best Local Similarity 33.8%; Pred. No. 13;
Matches 67; Conservative 35; Mismatches
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Location/Qualifiers
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                              May 31, 2000, 17:04:21; Search time 1292.59 Seconds (without alignments)
-918.913 Million cell updates/sec
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1221
1 cgcccgggcaggttgcatct.....aaattttatttttgctggta 1221
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Listing first 45 summaries
                      OM nucleic - nucleic search, using sw model
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Waterston, R.H.
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VERSION
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                                                                                                                                                                                  Length 548;
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                          PAT
                                                                                                                                                                                 Score 515.6; DB 5;
Pred. No. 2.3e-128;
1; Mismatches 7;
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                                                                                       1 (bases 1 to 548)
Yu.G. and Rosen.C.
Colon specific genes and proteins
Patent: US 5733748-A 6 31-MAR-1998;
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                                 5733748.
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128 c 173 g
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                       195745 548 bp DNA Sequence 6 from patent US 57 195745 153940215
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Best Local Similarity 98.2%;
Matches 540; Conservative
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Direct Submission
Submitted (11-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 178137)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                    Center project name: H_NH0475023.

* NOTE: This is a "working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is
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Biochimica ed Evoluzionistica, CNR, Via Abbiategrasso 207, 27100
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Bione, S., Tamanini, F., Maestrini, E., Tribioli, C., Poustka, A., Torri, G., Rivella, S. and Toniolo, D.
Transcriptional organization of a 450-kb region of the human
                                                                                                                                Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                       chromosome in Xq28 Proc. Natl. Acad. Sci. U.S.A. 90 (23), 10977-10981 (1993)
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Ab xref="taxon:9606"
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H.sapiens mRNA for 2.19 gene.
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Toniolo,D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (14-AUG-1996) to the DDBJ/EMBL/GenBank databases. Ikko
Ohno, Institute for Molecular and Cellular Biology, Osaka
University, Molecular Genetics; 1-3 Yamada-Oka, Suita, Osaka 565,
Japan (E-mail:Kousaku@imcb.osaka-u.ac.jp, Tel:81-6-879-7992,
Fax:81-6-877-1922)
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Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 2475)
                                                                                                                                                                                                                                                                                                                                gtgaaatteettaaagaaatteegggggggtgeactggtgetggtggeeteetaegaegat
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Ohno, I., Hashimoto, J., Takaoka, K., Ochi, T., Okubo, K. and
Matsubara, K.
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                                                                                                                                                                                                                                                                       DB 12; Length 465;
                                              /cell_line="NIH3T3"

/cell_type="Ed=-pbx1 induced fibroblasts"
complement(1)7. .>465)
/note="similar to human 2.19 protein"
                                                                                                                                                                                                                                                                                                  Indels
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complete cds.
                                                                                                                                                                                                                                                                                                  81,
                                                                                                                                                                                                                                                                    18.8%; Score 229.4; DB 1
llarity 77.4%; Pred. No. 2.9e-51;
Conservative 0; Mismatches 81
                                                                                                                                                                                                            ų
    musculus"
              /strain="BALB/c"
/db_xref="taxon:10090"
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GS3786,
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                                                                                                                                                                                                              109
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129 c
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GS3786.
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                                                                                                                                                                                                                                                                                                Matches 278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 ctcgcccaccaaggagatccaggttaaaaagtacaagtgtggcctcatcaagccctgccc 403
                                                                                                                                                                                            415 CTCGGTGACTGCAGCGCCACGGCCAGGAAGTACAAGTGTGGCCTGCCCCAGCCGTGTCC 474
                                                                                                                                                                                                                         404 agccaactactttgcgtttaaaatctgcagtggggccgccaacgtcgtgggccctactat 463
                                                                                                                                                                                                                                                    475 TGAGGAGCACCTGGCCTTCCGCGTGGTCAGCGGGCCGCCAACGTCATTGGGCCCAAGAT 534
                                                                                                                                                                                                                                                                                                               594
                                                                                                                                                                                                                                                                                                                                             categecettggtgaatggaaceaegggagetgtgetgggaeaggaaggeatttgaeatgta 583
                                                                                                                                                                                                                                                                                                                                                                   595 CATCGCCCTGGTGAACGGGGTCAGCGGCGTCATCGAGGCCCGGGCCTTTGACATGTG 654
                                                                                                                                                                                                                                                                                                                                                                                                      ctetgacttggggagttcctacgcaaacaactgggcttccgggacagctgggtcttcat 763
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W.X. and Kamps, M.P.
E2a -PAz1 induces aberrant expression of tissue-specific and developmentally regulated genes when expressed in NIH 3T3
                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                        Length 1606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; I
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USA
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Fu,X. and Kamps,M.P.
Fu,X. and Kamps,M.P.
Submission
Submitted (27-SEP-1996) Pathology, University
Diego, 9500 Gilman Drive, La Jolla, CA 92093,
Locatlon/Qualifiers
1.465
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                                                                                                     Score 247.8; DB 9;
Pred. No. 3.1e-56;
; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Cell. Biol. 17 (3), 1503-1512 (1997)
97184476
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partial cds
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Mus musculus EF-7 mRNA,
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66.2%;
                              1588. .1593
521 c
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                                                                                                     Query Match 20.3
Best Local Similarity 66.2
Matches 357; Conservative
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                              polyA_signal
BASE COUNT 301
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join(3351. ;3470,13327. ;13364,13460. ;13568,14118. ;14335,
15007. ;15165,15343. ;15468,15834. ;15927,16375. ;16561,
16701. ;16936,17041. ;17117,17223. ;17315,17413. ;17503)
/gene="G6PD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="pim by Tom Vulliamy"
1. 20111
/note="1-2011 bp replaces previous submission X55448,
1-20114 bp; 6 corrections made from X55448, including 8850
(delete T), 14575 (add C), 18788 (delete C), 19369 (delete G), and 19480 (T changes to A); G6PD:
Glucose-6 phosphate Dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="maeqvalsfrqvcgilreeleqgdaffqsdfhffimgasgdla
kkryptymulfrdgileenyfimgyarsritvadirkosepferatpeekikledef
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qigmyriyekpfeydqsdsyblishissleredqirtibhilgermyqnimulrean
Rifgpiwnrdiacvilifrkepfgtegrggypdefgilirdvwqnhllqmcluvamekp
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ATFAAVLLYVENERWDGVPFILRCGKALNERKAEVRLQFHDVAGDIFHQCKRNELVI
RVQPNERAVYTKMMTKKPOMFRNEESELDLTYGNRYKNVKLPDAYERLLIDVFCGSQM
HFVRSDELREAMRIFTPLLHQIELEKPRPIPYIYGSRGPTEADELMKRVGFQYEGTYK
WVNPHKL"
                Eukaryotta Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Prinates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 52173)
2010,M., Mazzarella,R., Bione,S., Toniolo,D., Schlessinger,D., Sequence and Chen,B.Y.
Sequence and gene content of the RCP/GCP-GGFD region in human Xq28: the first 52kb
                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-7AN-1994) Ellson Y Chen Dr., Advanced Center for Genetic Technology, Applied, Biosystems Division, Perkin Elmer Corp., 850 Lincoln Centre Drive, Foster City, CA, 94404, USA On Jan 26, 1994 this sequence version replaced 91:31540.
                                                                                                                                                                                                                Green, P.,
                                                                                                                                                                                      2 (bases 1 to 20111)
Chen, T. Y. (Cheng, A., Kuang, W.J., Hillier, L., Green, P.,
Schlessinger, D., Ciccodicola, A. and D'Urso, M.
Sequence of human glucose-6-phosphate dehydrogenase cloned in
plasmids and a yeast artificial chromosome
Genomics 10 (3), 792-800 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="glucose-6-phosphate dehydrogenase"
/protein_id="CAA39089.1"
/db_xref="G1:452269"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .52173
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=experimental
2255. . 18112
/gene="66pD"
3343. .3470
/gene="66pD"
/citation=[2]
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="Cosmid TV1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="G6PD"
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2252. .2717
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    sapiens
                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                              /codon_start=1
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/product="c(S3786"
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/translation="MRYAGAAKLVVAVAVFILTFYVISQVFEIKMDASLGNLFARSAL
GINVALANGKTGFVLDTKYFDWMGGDVAFFIEFLEKALGDGTYLDGATYLNUGR
GINVALANGKTGFVLDTKYFDWMGGDVAFFIEFLEKALGDGTYLDGATYLNUGR
ARRLIADLGSTSITNLGFRDNWVFCGGKGIKTKSPFEQHIKNNKDTNKYFGWPEVVEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggggccgccaacgtcgtgggccctactatgtgctttgaagaccgcatgatcatgagtcct 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaaatgaacgatgaaagcaggaaactcttctctgacttgggggagttcctacgcaaaacaa 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cttaaagaaattccgggggggggctgctggtggtggctcctacgacgatccagggacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tttgagcagttcttaaagaacagcccagacacaaacaaatacgagggatggccagagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 GGAGCAGCCAACGTGGTGGGACCCAAAATCTGCCTGGAAGATAATGTTTTAATGAGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  573 CIGAAGCCATACAAGATGGAACAATAGITTTAATGGGAACATACGATGATGGAGCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACTCAATGATGAGGCACGCGCCTCATTGCTGATTTGGGGAGCACATCTATTACTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 216.4; DB 9; Length
Pred. No. 8.9e-48;
0; Mismatches 196; Indels
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Best Local Similarity 63.0%;
Matches 334; Conservative (
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ö Gaps ; 0 Query Match 5.7%; Score 70; DB 9; Length 52173; Best Local Similarity 68.3%; Pred. No. 2.3e-08; Matches 97; Conservative 0; Mismatches 45; Indels ŏ

RESULT 7 HUMFLNG6PD/C LOCUS HU QQ

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HUMFLNG6PD 219447 bp DNA PRI 17-MAY-1999 Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds/s. L44140 GI:1203968 ACCESSION VERSION

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	OKUANISM HOMO Saptens Eutheria: Metazoa: Chordata; Craniata; Wertebrata; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo. REFERENCE (bases 1 to 2194A) AUTHORS Chen, E. Y., Zollo, M., Mazarella, R. A., Ciccodicola, A., Chen, CN., Zuo, L., Heiner, C., Burough, F. W., Ripetto, M., Schléssinger, D. and	D'Urso, M. TITLE Long-range sequence analysis in Xq28: thirteen known and six candidate genes in 219.4 kb of high GC DNA between the RCP/GCP and G6PD loci Genet. 5 (5), 659-668 (1996) MEDLINE 96711563		id Schlessi artment of icine hington Uni Louis MO ail: ellsor e: Gene pre	1.1 and 1.2, coupled with fasta and blastx comparisons to genbank s non-redundant peptide libraries. Repeat analysis was accomplished via	FEATURES censor. Location/Qualifiers source 1219447 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="X"	/map=-X- repeat_unit 422=-X- /rpt_family="Alu-Sp or Alu-Sq" /rpt_family="Alu-J or Alu-Sq" /rpt_family="Alu-J or Alu-S" /rpt_family="Alu-J or Alu-S"		g o	repeat_unit complement(36633952) /rpt_family="Alu-sb0 or Alu-sb1" /evidence=experimental /evidence=experimental /rpt_family="Alu-sb or Alu-s" /rpt_family="Alu-sb or Alu-s" /evidence=experimental /rpt_family="Alu-sb0 or Alu-sb1" /evidence=experimental /evidence=experimental /evidence=experimental /evidence=experimental

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YTPYEEGLHSVDVIYDGSPVPSSPFQVPVTEGCDFSRVRVHGPGIQSGTINKPNKFTV
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EPVDVVDNADGTQTVNYVPSREGPYSISVLYGDEEVPRSPFKVKVLPTHDASKVKASG
                                                   complement(18984. .45006)
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                                                                                                     Db 177752 CCATGCTGCAGGATGAATGAAGAGACAGAAAGCTCTTCAGTGAGCTGGGCAGCAGGAAC 177693
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                                                                                                                                                        726 gcaaaacaactgggcttccgggacagctgggtcttcataggagccaaagacctcaggggt 785
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                                            45; Indels
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Pred. No. 2.3e-08;
0; Mismatches 45;
  5.7%;
Query Match
Best Local Similarity 68.39
Matches 97; Conservative
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786 aaaagccctttgagcagttct 807

AC006364 132319 bp DNA PRI 21-DEC-1999 Homo sapiens BAC clone GS1-146J4 from 7q31.1-31.3, complete Db 177632 AAGAGCCCCTTTGAGCAGGTAT 177611 sequence. LOCUS DEFINITION æ RESULT ACO06364 ACCESSION

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Waltsburn, Cubmission
Submitted (21-DEC-1999) Department of Genetics, Washington
Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On May 5, 1999 this sequence version replaced gi:4337266.
                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (11-JAN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (05-MAY-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (11-SEP-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 132319)
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                    2 (bases 1 to 132319)
Ryan,E., Bauer,C., Tucci,S. and Spalding,L.
The sequence of Homo sapiens BAC clone GSI-146J4
                                                                                                                                                                             Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                 1 (bases 1 to 132319)
Sulston, J.E. and Waterston, R.
  AC006364.3 GI:4753253
                                                                                                                                                                                                                                                                                                            Unpublished
3 (bases 1 to 132319)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (bases 1 to 132319)
Waterston, R.H.
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                                                                     Homo sapiens
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                                           SOURCE
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu

Center code: WUGSC

Center project name: H_GS146J04

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov, or see http://genome.wustl.edu/gsc

This clone is from the first BAC library from Genome Systems, Inc. (http://www.genomesystems.com). SOURCE INFORMATION:

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//note="similar to EST AA897626 (NID:g3034240) oj71h05.s1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349 ccaccaaggagatccaggttaaaaagtacaagtgtggcctcatcaagcctgcccagcca 408
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Sequence 14 from patent US 5670367.
166494
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166494/c
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/gene="WUGSC:H_GS146J04.1"
join(11713. .11725.15668. .15772,22543. .22572,23259. .23382,
30494. .30552,31735. .31785,34555. .34639,43413. .43539,
44432. .44221)
/gene="WUGSC:H_GS146J04.1"
/note="match to Q92520 (PID:g3334194); H_GS146J04.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mryagaaklvvavavellffyvisovfeikmdaslgnlfarsal
DTAARSTKPRYKGGISKACPEKHFRFKMASGAANVGPKICLEDNVAMSGVKNNVGR
DIVALANGKTGEVLDTKTPDWGGDVAPFIEFLKALODGTYVLMOGTYDDGATKLNDE
ARRLIADLGSSTSITHUGFRDNWYFCGGKGIKKRSPFEQHIKNNKDTNKYEGWPEVVEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11665. .11725
/note="similar to Mus musculus EST AA986059 (NID:g3167448)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match to EST H18852 (NID:g885092) ym45f11.r1"
10754. .11029
/note="match to EST AA328782 (NID:g1981047)"
11459. .11522
//rpt_family="L2"
11660. .1214
//octe="similar to EST AI220397 (NID:g3802600) qg73h11.x1"
                  Haplotypes: two
VECTOR: pBeloBAC
Selection: chloramphenicol
NEIGHBORING SEQUENCE INFORMATION:
The actual start of this clone is at base position 1 of GS1-146J4;
actual end is at 132319 of GS1-146J4.
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7983. 8089

8111. 8253

7Ppt_family="Retroviral"

10366. 10769

10401. 10850
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/rpt_family="MER1_type"
7930. .7982
/rpt_family="Retroviral"
                                                                                                                                                           /organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosom="7"
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/clone="151-4654"
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/rpt_family="12"
/rpt_family="1516"
/rpt_family="1516"
/rpt_family="1516"
/rpt_family="1516"
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/db_xref="G1:5870323"
                                                                                                                                                                                                                                                                                                                                                                                                                1512. .2783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="POLY_G"
3880. .4030
/rpt_family="MER1_type"
4108. .4397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="Retroviral"
413. .6446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="(TGGA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="(CA)n"
                                                                                                                                                                                                                                                                                                                                                            /rpt_family="L1"
2118, .2474
/rpt_family="MaLR"
2512, .2783
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   lymphoblastoid
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Worley, K.C.
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Eutheria; Primates; Catarrhin; Hominidae; Homo.
Eutheria; Primates; Catarrhin; Hominidae; Homo.
E I (bases 1 to 3505)
E Muzzy, D. M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,
Bodcta, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C.,
Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
Dugan-Rocha, S., Durbin, K. J., Fernandez, C., Ferraquto, D.,
Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J. L.,
Guevara, M., Harris, K., Hernandez, J., Hodgson, A., Hogues, M.,
Holloway, C., Hosak, H., Jackson, L. E., Jackson, L., Jia, Y., Jones, M.,
Kelly, S., Kondejewski, N., Rong, Y., Kovar, C., Leal, B., Li, Z.,
Lichtarge, O., Liu, J., Liu, W., Logado, N.P., Mei, G., Morgan, M.,
Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M.,
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Homo sapiens clone RP11-90809, *** SEQUENCING IN PROGRESS ***, 30
unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                          gacgatccagggaccaaaatgaacgatgaaagcaggaaactcttctctgacttggggagt 719
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                                                                                                                                                                                                                                                                                                                                                                     480 atgatcatgagtcctgtgaaaaacaatgtgggcagaggcctaaacatcgccctggtgaat 539
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                                                                                                                                                                                                                      368 others
                                                                                                                                                                                                                                                                                             Score 46.6; DB 5; Length 7
Pred. No. 0.048;
13; Mismatches 177; Indels
                                                                                       1 (bases 1 to 7218)
Dorner, Schefflinger, F. and Falkner, F. Gunter.
Dorner, Compox virus
Patent: US 5670367-A 14 23-SEP-1997;
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                                                                                                                                                            Location/Qualifiers
1. .7218
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HTG; HTGS_PHASE1.
GI:2724471
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Best Local Similarity
Matches 25; Conserv
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I66494.1
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Center: Baylor College of Medicine
Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu
Web Site: http://www.hgsc.bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: HMKR
Center clone name: RPI1-90809
Sequencing vector: M13: LO8821
Chemistry: Dye-terminator B19 Dye: 99% of reads
Assembly program: Phrap; version 0.980611
Consensus quality: 12430 bases at least Q40
Consensus quality: 19864 bases at least Q30
Consensus quality: 2369 bases at least Q30
Estimated insert size: 35052; agarose-fp estimation
Estimated insert size: 24454; sum-of-contigs estimation
Quality coverage: 0.3x in Q20 bases; sum-of-contigs estimation
Quality coverage: 0.5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                         Direct Submission Submission Submitted (23-NOV-1999) Human Genome Sequencing Center, Department Submitted (23-NOV-1999) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Feb 19, 2000 this sequence version replaced 91:6466486.
Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S., Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L., Oswal, G., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sucqanq, R., Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wahbah, M., Watlington, S., Weinstock, G., Weinstock, I.R., Williamson, A., Woley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and
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of 1096 bp in length
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of 1252 bp in length
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of 1063 bp in length
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Location/Qualifiers
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217 c 179 a
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Zhou,S., Liu,M. and He,F.
Functional prediction of the coding sequences of 50 new genes
deduced by analysis of cDNA clones from human fetal liver
Unpublished
2 (Dases 1 to 1302)
2 (Dases 1 to 1302)
3 (Pases 1 to 1302)
4 (Pases 1 to 1302)
5 (Pases 1 to 1302)
6 (Pases 1 to 1302)
7 (Pases 1 to 1302)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1302)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%; Score 43.4; DB 57; Length 35052; 79.0%; Pred. No. 0.34; tive 0; Mismatches 16; Indels 1;
si contig of 1302 bp in length
si gap of unknown length
contig of 1865 bp in length
contig of 1190 bp in length
contig of 1190 bp in length
contig of 1230 bp in length
contig of 1180 bp in length
gap of unknown length
contig of 1865 bp in length
gap of unknown length
contig of 865 bp in length
gap of unknown length
contig of 885 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 181 bp in length
gap of unknown length
contig of 1531 bp in length
gap of unknown length
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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9047 c 7874 g
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Homo sapiens clone HQ0688.
AF090946
AF090946.1 GI:6690254
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31525:
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16603:
16623:
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29346:
29366:
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25472:
26950:
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Best Local Similarity 79.09
Matches 64; Conservative
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22436
23902
23922
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32877
32897
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114529
115394
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116604
116624
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SOURCE
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AF090946
LOCUS
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Linguistic Submission

Submitted (03-FEB--7000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Feb 16, 2000 this sequence version replaced gi:6911686.

IMPORTANIT This sequence is unifinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Contig_ID: 01063 Length: 50802bp

Contig_ID: 01189 Length: 1055bp

Contig_ID: 02238 Length: 1155bp

Contig_ID: 0224 Length: 1155bp

Contig_ID: 0224 Length: 1105bp

Contig_ID: 0224 Length: 1105bp

Contig_ID: 0224 Length: 1105bp

Contig_ID: 04132 Length: 1039bp

Contig_ID: 04132 Length: 1039bp

Contig_ID: 04131 Length: 1103bp

Contig_ID: 04137 Length: 1203bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538 atggaaccacgggagctgtgctgggacagaaggcatttgacatgtactctggagatgtta 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       598 tgcacctagtgaaattccttaaagaaattccgggggggtgcactggtgctggtggcctcct 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       658 acgacgatccagggaccaaaatgaacgatgaaagcaggaaactcttetetgacttgggga 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           665 YKRWKGKYCMWKSMMSSMMSTYMWYYKGGSCYKSMRKKRAAAARKWMTYYWRKTKGRKK 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Direct Submission
Submitted (10-SEP-1998) Dept. of Experimental Hematology, Beij
Institute of Radiation Medcine, 27 Taiping RD, Beijing 100850,
P.R.China
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 173823)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 3.5%; Score 43; DB 51; Length 1302; Best Local Similarity 12.0%; Pred. No. 0.45; Matches 28; Conservative 115; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                167 others
                                                                                                                                                                                                                                                                                                                                                                                لد
                                                                                                                                                              1. .1302
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HQ0688"
/tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                415
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11-FEB-2000 SEQUENCING IN

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Submitted (10-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, Wr. E-mail enquiries: humquery@anger.ac.uk Clone requests: clonerequest@anger.ac.uk humquery@anger.ac.uk Clone requests: clonerequest@anger.ac.uk

On Feb 16, 2000 this sequence version replaced gi:6977930.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Contig_ID: 00059 Length: 1135bp Contig_ID: 01376 Length: 1132bp Contig_ID: 01376 Length: 1132bp Contig_ID: 01376 Length: 1132bp Contig_ID: 03101 Length: 1552bp Contig_ID: 03101 Length: 1502bp Contig_ID: 03101 Length: 1502bp Contig_ID: 03101 Length: 1502bp Contig_ID: 03101 Length: 48632bp Contig_ID: 03101 Length: 48632bp Contig_ID: 03101 Length: 48632bp contig_ID: 03101 Length: 48632bp contig_ID: 03101 Length: 48034pp.

* NOTE: This is a 'working draft' sequence record is anbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 123645)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7593 8392; gap of 800 bp
8393 9515; contig of 1123 bp in length
10316 58947; contig of 48632 bp in length
58948 59747; gap of 800 bp
59748 74811; contig of 15064 bp in length
74812 75611; gap of 800 bp
75612 123645; contig of 48034 bp in length.
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1316 2115; gap of

1316 3123; contig of 1123 bp in length

1329 4038; gap of

1339 5590: contig of 1552 bp in length

5591 6390; gap of

6391 7592: contig of 1202 bp in length
                                                                                                                                  clone RP4-697K14,
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/clone_lib="RPCI-4"
35331 c 34990 g 23221 t
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/db_xref="taxon:9606"
                                                                                                                                     Homo sapiens chromosome 20 clone
PROGRESS ***, 8 unordered pieces.
                                                                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                             AL121829.8 GI:6983416
                                                                                                            HSJ697K14 123645 bp
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                                                       RESULT 13
HSJ697K14/C
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KEYWORDS
SOURCE
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Contig_ID: 04138 Length: 1158bp
Contig_ID: 04108 Length: 1427bp
Contig_ID: 04214 Length: 9238bp
Contig_ID: 04214 Length: 3772bp
* NOTE: This is a "working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 33; Length 173823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149198 149997; gap of 100 bp 149998 151036; contig of 1039 bp in length 151037 151836; gap of 800 bp 151837 151836; gap of 800 bp 151837 153025; contig of 1189 bp in length 153026 153825; gap of 800 bp 1518326 155829 156986; contig of 1139 bp in length 155829 156986; contig of 1158 bp in length 155829 155928; gap of 800 bp 157786; gap of 800 bp 157787 159213; contig of 1427 bp in length 159214 160013; gap of 800 bp 160014 1695213; contig of 200 bp 160014 1605213; contig of 200 bp 160014 1605213; contig of 200 bp 160014 1605213; contig of 200 bp 160014
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44243 c 44350 g 35714 t 12017 others
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Pred. No. 0.43;
0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                         100 bp
50802 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127104 127903: gap of 800 bp
127904 141008: contig of 13105 bp in length
141009 141808: gap of 800 bp
141809 143640: contig of 1832 bp in length
145841 144440: gap of 800 bp
144441 149197: contig of 4757 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139: gap of 800 bp
124798: contig of 58359 bp in length
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f 1175 bp in length
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2115 12062: contig of 9948 bp in length
12063 12862: gap of 800 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124799 125598: gap of 800 bp 127103: contig of 1505 bp in length
                                                                                                                                                                                                                                                                                                              1314: contig of 1314 bp in length
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63664: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of
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64465 65639: cont
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Local Similarity 53.0%;
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                               Gaps
   Length 123645;
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                             Indels
Score 41.4; DB 33;
Pred. No. 1.2;
0; Mismatches 136;
Query Match 3.4%;
Best Local Similarity 47.5%;
Matches 123; Conservative
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AL Submission

Birect Submission

AL Submisted (03-FBB-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Feb 16, 2000 this sequence version replaced gi:6911627.

IMPORTANT: This sequence version replaced gi:6911627.

IMPORTANT: This sequence work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Contig_1D: 02382 Length: 1116bp Contig_1D: 02583 Length: 1110bp Contig_1D: 02687 Length: 1110bp Contig_1D: 02687 Length: 1110bp
                                                                                                                                                                                                                                                                                   77783 GGGGTGTCCCGAGTCTCAGGGGCTGGGGGCAGGCGGCCGTCGGGTGCAGGTGGGGGTCA 77724
                                                                                                                             CGGCAGGGCTCACTCAGGCATGAGTCGGGAGAAGGGAGGCCAGCTGGAAGGGGGCCAGGGG 77664
                                                                                                                                                                      959 ccggcaggggttgaggaggaggagcagggggtgctgcgtggaaggtgctgcaggtccttg 1018
                                                                                                                                                                                                              cacgetgtgtcgcgcctctcctccggaaacagaacctcccacagcacatcctacccg 1078
839 gggatggccagagctgctggagatggaggctgcatgcccccgaagccattttagggtgg 898
                                                                                     HSDJ663D7 185436 bp DNA HTG 03-FEB-2000 Homo sapiens chromosome 20 clone RP4-663D7, *** SEQUENCING IN PROGRESS ***, 25 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 189436)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 1526bp
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                                                                                                                                                                                                                                                                                                                                                                         77543 GCCCCTGGCGTCCGTGTG 77525
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AL121907.14 GI:6982672
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                             1079 gaagaccagcctcagaggg 1097
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Contig_ID: 03912
Contig_ID: 03952
Contig_ID: 03994
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HSDJ663D7/C
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21732 GGGGTGTCCCGAGTCTCAGGGGCTGGGGGCGCAGGCGGCGCGCGGTGGAGGTGGGGGGTCA 21673
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                    1: contig of 3889 bp in length
gap of 800 bp
gap of 800 bp
gap of 800 bp
3: contig of 1375 bp in length
3: contig of 1356 bp in length
6: contig of 1526 bp in length
6: contig of 1526 bp in length
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f 9323 bp in length
800 bp
f 3274 bp in length.
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1103 bp in length
800 bp in length
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33782 a 49857 c 48991 g 33600 t 19206 others
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                                                                                                          contig of 1216 bp in length of 800 bp contig of 1110 bp in length contig of 1110 bp in length
                                                                                                3719: contig of 3719 bp in length
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3.4%; Score 41.4; DB 33;
Best Local Similarity 47.5%; Pred. No. 1.2;
Matches 123; Conservative 0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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151585 154757: contig of
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134742 141871: contig of
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146896 150784: contig of
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172040 181362: contig of
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181363 182162: gap of
182163 185436: conți
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132839 133941: cont
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4520 5735: co
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The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Details of leishmania sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL132763.1 GI:6165382
GGG-related protein kinase, DNA replication licensing factor MCM4,
drug resistance protein; GlO protein homologue; heat shock protein
HSLU; integral membrane protein; sodium stibogluconate resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           see http://www.sanger.ac.uk/Projects/L_major/
CDS are numbered using the following system eg L4768.01. L4768
(cosmid name). .01 (first CDS)
To make the cosmid library Leishmania major Friedlin DNA was
partially digested with Sau3A1 prior to cloning into BamHI site of
the cosmid shuttle vector cLHYG (Ryan et al. 1993 Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 30:157-166(1984) as implemented at http://www.nih.go.jp/
jun/cgl-bin/frameplot.pl/ (2)
codon preference based on the codon usage table for Leishmania at http://www.kazusa.or.jp/codon/
                                                                                                                                                                                                                                                                                                     11552 CCTGTGGCCCTTGGCCCCAGCGCCATGCGCCTTCCAGGCCGCACCTTGCCTTGCCT 21493
                                                            21672 CGCCAGGGCTCACTCAGGCATGAGTCGGAGAAGGGAGGCCAGCTGGAAGGGGGCAGGGG 21613
                                                                                                                               959 ccggcaggggctgaggaggaggagcagggggtgctgcgtggaaggtgctgcaggtccttg 1018
                                                                                                                                                                                                                                                              cacgetgigicgedectetectecteggaaacagaaceteceacageacatectaceeg 1078
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15-DEC-1999
                                                                                                                                                                                       Leishmania major
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMFL4768 40969 bp DNA INV 15-
Leishmania major Friedlin chromosome 23 cosmid L4768.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    21492 GCCCCTGGCGTCCGTGTG 21474
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1 (bases 1 to 40969)
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ACCESSION
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KEYWORDS
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// Note="fregion of BlaSTN similarity to bases 89666. .89790 208556 Plasmodium falciparum MR13P7; 62% identity over 124 bases; region of BlaSTN similarity to bases 5. .192 AA547848 WB3D6V160973 Brugia malayi day 6 post-infection third stage larvae SAM96MLM-BmL3d6 Brugia malayi CDNA clone 3D6V1609 5; 69% identity over 106 bases" complement(618. .731)
// Note="region of BlaSTN similarity to bases 67. .180 AA547848 WB3D6V160973 Brugia malayi day 6 post-infection third stage larvae SAM96MLM-BmL3d6 Brugia malayi cDNA clone 3D6V1609 5; 69% identity over 113 bases; region of BLASTN similarity to bases 121. .192 AA647848 WB3D6V1609T3 Brugia malayi day 6 post-infection third stage larvae SAM96MLM-BmL3d6 Brugia malayi cDNA clone 3D6V1609 5; 76% identity over 71 bases 121. .192 AA647848 WB3D6V1609T3 Brugia malayi cDNA clone 3D6V1609 5; 76% identity over 71 bases.
                                                                                                                                                                                                                                                                                                                                                                                                          CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (acg) which is preceded by a stretch of pyrimidines or part of a Kozak sequence. If this cannot be identified we choose the most upstream initiation codon.
the Hexamer program which was written by Richard Durbin as an integral part of the ACEDB-based analysis tools for the C-elegans Genome Sequencing Project. The program calculates the 109-11Kellhood score for a given DNA segment based on the frequency of 6-mers, normalised for the base-pair composition of the genome. The program was trained using a fasta file of confirmed Leismania major coding sequences (CDS), i.e. from ATG start codon to the stop
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/gene="L4768.01"
/gene="L4768.01"
/gene="L4768.01"
/note=="L4768.01"
Fonce="L4768.01"
Fonce="L4768.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane domains were predicted as implemented at the TMHMM server: http://www.cbs.dtu.dk/services/TMHMM-1.0/
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid L4768 does not overlap any sequenced cosmids to date.
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AC010851 Leishmania major chromosome 22 clone L4134,
complete sequence.; 64% identity over 116 bases"
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/note="cecececececetectectetetecececec"
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/strain="Friedlin"
/db_xref="taxon:5664"
/chromosome="23"
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/note="ccccctctccccttctcc"
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complement(316. .330)
/note="ttccccctctccct"
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/note="(gcat)3"
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5;

/product="possible cdc2-related protein kinase'

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complement(5335. 5777)

// Gene="L4768.02"

// Complement(5335. 5777)

// C
similarity to Y401_LAMBD, hypothetical protein orf401. (401 as, Bacteriophage lambda, EMBL: J02459, AAA96555); Fasta scores: E():0.012, 28.5% identity in 249 as" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2104. .2142)
/gene="L4768.01"
/note="PROSITE PS00094 C-5 cytosine-specific DNA
methylases active site, info count = 22.3"
/gene="L4768.01"
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/protein_id="Ca859858.1"
/db_xref="GI:6165383"
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/note-"ccccttctccccc"
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complement(3505. .3573)
/gene="L4768.01"
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/note="cccttttctctctctctctt"
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/label=cctctccctcctcccomplement(4491. .4508)
/note="(cccat)3"
/label={cccat}3
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/note="tecctcctcttcctc"
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/codon_start=1 /label=L4768.02

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17758 GCGCATGAAGGATCGCCTGCGCTACCTGGTGCGTGCCTGTGCGCCTGTCTCTC 17816
                                                                                                                                                                                                                                                                        17877 GGAGGAGGAGGAGGAGGAGGCAAAGGTGATTCAGCACCACCACCCTTTTTCTTTGG 17936
                                                                                                                        17698 TTGAGCATCGGCAAAAGGAAAAAGGAAAGCACGTGCGCTGGTGTGTGAGACCGTC 17757
                                                                                                                                                                                                                                                                                                                                  ggaggagcagggggtgctgcgtgg--aaggtgctgcaggtccttgcacgctgtgtcgcgc 1033
                                                                                                                                                                856 tggagatggagggctgcatgccccgaagccattttagggtggctgtggctcttcctcag 915
                                                                                  796 ttgagcagttcttaaagaacagcccagacacaaacaaatacgagggatggccagagctgc 855
                                              Gaps
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                                            3;
      Length 40969;
                                              Indels
Query Match 3.3%; Score 39.8; DB 34; Best Local Similarity 49.5%; Pred. No. 3.2; Matches 157; Conservative 0; Mismatches 157;
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Job time: 5575 sec
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